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AF363055 AF363056 AF163833 AF332897 AF332899 AF332899

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AX602206 SAG766849 AF332895

AY375362 AB028896 AF332901

Sequence

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AF337958 AF367973 AF363035

AF363032 AF363033 AF363034 AF363038

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AF363038 AF363039

ALIGNMENTS

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AF155804 Streptococcus suis strain 6555 Cps1E (cps1E) gene, partial cds; Cps2F (cps2F), Cps1G (cps1G), Cps1H (cps1H), Cps1I (cps1I), and Cps1J (cps1J) genes, complete cds; and Cps1K (cps1K) gene, partial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (02-7UN-1999) Bacteriology, Animal Science and Health, P.O. Box 65, Lelystad 8200 AB, The Netherlands Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptococcus.

1 (bases 1 to 6992)

Smith, H.B., Damman, M., van der Velde, J., Wagenaar, F.,
Wisselink, H.J., Stockhofe-Zurwieden, N. and Smits, M.A.
Identification and characterization of the cps locus of
Streptococcus suis serotype 2: the capsule protects against
phagocytosis an important virulence factor
Infect. Immun. 67 (4), 1750-1756 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Smith, H.S., Veenbergen, V., van der Velde, J., Damman, M., Wisselink, H.J. and Smits, M.A.
The cps genes of Streptococcus suis serotypes 1, 2, and development of rapid serotype-specific PCR assays J. Clin. Microbiol. 37 (10), 3146-3152 (1999)
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Streptococcus suis
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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Smitch.H.E., Veenbergen,V., Van der Velde,J., Damman,M.,
Wisselink.H.J. and Smits,M.A.
Direct Submission
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JOURNAL
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AX083715 Sequence
AZ8876 S.preumonia
AY376403 Streptoco
AF149539 Streptoco
AF14245 Streptoco
AF04245 Streptoco
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AF363057
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                                                                  April 28, 2005, 15:47:38; Search time 28553 Seconds
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           GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
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                                                 - nucleic search, using sw model
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1501 AGANTGAAAAATGTRICCATGAAATTTICCACAAATCGCAATCTCATTAATTTAGTG 1560 1561 AAAATGCTRICCATGACAATTTICCACAAATCCCAATCGCAATCCCATTTAATTTTCAT 1520 1561 AAAATACTTICCAAAATTTTACACTCATACAAAAACCAAATGTTAATTTCAT 1520 1621	
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1721 TTGCTTGGGGTAMAMAGCTAATAGTAATATTGGAATACTACTAATATTGAATACTGGGGGGGG	
8 4 5 8 5 8 5 8 5 8 5 8 5 8 5 8 5 8 5 8	-
2561 ACTOTTHGANTTHATTATANGANTGENECRACTHTTGANTCHATTACAMGANTGETT 2640 2641 GITTATTGANTGANTAMAMACHGETCHAGANTAGANTHGANTTGGANTGGANTGGANTGGANTGGA	7.0 14449010044444490100100100100100100100000000

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5	6 B 6 B 6
4801 GANTINITITITITITITITITITITITITITITITITITI	

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determination/export"
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                                                                                                                                                                            Streptococcus suis Cps2A (cps2A), Cps2B (cps2B), Cps2C (cps2C), Cps2D (cps2D), Cps2E (cps2E), Cps2E (cps2E), Cps2B (cps2C), Cps2B (cps2E), Cps2B (cps2C), Cps2B (cps2B), Cp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (07-JAN-1999) Department of Bacteriology, DLO-Institute for Animal Science and Health, P.O. Box 65, Lelystad 8200 AB, The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptococcus.

1 (bases 1 to 15401)

Smith, H.B., Damman, M., van der Velde, J., Wagenaar, F., Wisselink, H.B., Damman, M., van der Velde, J., Wagensar, F., Wisselink, H.G., Stockhofe-Zurwieden, N. and Smits, M.A. Identification and characterization of the cps locus of Streptococcus suis serotype 2: the capsule protects against phagocytosis and is an important virulence factor Infect. Immun. 67 (4), 1750-1756 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptococcus suis
Bacteria, Firmicutes, Lactobacillales, Streptococcaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 (bases 1 to 15401)
Smith, H.E., Damman, M., van der Velde, J., Wagenaar, F.,
Wisselink, H.J., Stockhofe-Zurwieden, N. and Smits, M.A.
Direct Submission
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TTAVLEGIYLKRKLKLKLPLLWHYHEIIYKPKFISDSINPLMGRFADKU VTVSQAVANHI
KQSPHIKDOJISVIYNGVDNKVFYQSDARSVPERFDIDEEALVIGMVGRVNAWKGQGD
FLEAVAPILEGNPKALAFIAGSAFEGEEWRYVELEKKISQLKKVSSQYRRMDYTTE
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LANESKVILQLSENINLRKKIGNNSIERQKEHFSLKSYVKNFSKVYTSLKVY"
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NSAKSDITGEVFEHNCATCFNIDVPNIGSAKAILYDIMALKKSIEIAKDRNDTSPIFY
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Bacteria, Firmicutes, Lactobacillales, Streptococcaceae,
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1 (bases 1 to 17468)
Stallu, F., Ehrlich, D.S. and Renault, P.
Diversity of ps operons in Streptococcus thermophilus Unpublished
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Rallu,F., Ehrlich,D.S. and Renault,P.
Direct Submission
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/note="Eps3K; putative glucosyltransferase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
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                                                                                                                  9374. .10474
/gene="eps3J"
9374. .10474
/gene="eps3J"
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/gene="eps3K"
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65.8%;
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                                                                                                                                                                                 /protein_id="AAL23730.1"

/db_xref="G1:24473739"

/db_
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EKMYSCHFPTNRNLKNLIKNTFLAIKVLKKEKPDVIISSGAAVAVPFFYIGKLFGAKT
VYIEVFDRIDKPTVTGKLVYPVTDKFIVQWEEMKKVYPKAINLGSIF"
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KFCQMSRLISFDQMSKFMQKADIIITHGGPATFMSAITWGKKPIVVPRQEKFGEHVND
HQVDFARNVAKRMGTIILVBDVDKLGETIENYNSIVAELBYDMGNNNKKFNKDLEGIV
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/db_xref="G1:24473742"
/translation="MNYAKTCFLIIAHNNWGQLKKLIECLDSQTHDIFVHVDKKSKDF
DESYFIDSVTKSSLKFYREFTVYWGDFSQVQVEMFLLEQAYIEGYDYYHIISGADLPL
                                       note="undecaprenylphosphate glucosyltransferase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="putative galactosyltransferase enhancer"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1275. .7647
/gene="eps3F"
/note="Eps3F; putative undecaprenylphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note="Orf3A; putative rhamnosyltransferase"
pseudo
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db_xref="GI:24473741"
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db_xref="GI:24473740"
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/pseudo
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/transl_table=11
6275. .7647
/gene="eps3F"
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/transl_table=11
7682..8131
/gene="eps3G"
                                                                                                          transl_table=11
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/product="eps3H"
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/gene="orf3A"
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/gene="eps3H"
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'gene="orf3A"
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gene="eps3G"
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/gene="eps31"
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/gene="eps3I"
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                              8021 CCAACAGTTACAGGAAAATTAGTGTACCCTGTGACGGATAAGTTCATTGTTCAATGGGAA
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Patent: WO 0179500-A 9 25-OCT-2001;
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COMPAGNIE GERVALS-DANONE (FR); Rhodia Chimie (FR)
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8501 TAGATAAATTGGGGGGGGCTATTGAAAATTACAA 8534
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EHIKDFGSTLNTGHWHGDMPGLSDKAVVLATSKGYPHQIICFSPKHYAFQAHLEFDLE
AIDLLIAADGEEHLYQQNKQLDFVQTPEQLHNHDYSQMNKKLFAFLDSLTQI"
                                                                                                                            BCT 04-JAN-2002
                                                                                                                                                                                                                                                                                                                                                             deoD gene; DeoD protein; Eps 2; Eps 3; Eps 4; eps10 gene; Eps10 protein; eps12 gane; Eps12 protein; eps12 gane; Eps12 protein; eps14 gene; Eps14 protein; eps15 gene; Eps14 protein; eps15 gene; Eps15 protein; eps16 gene; Eps16 protein; eps2 gene; eps3 gene; eps3 gene; eps3 gene; Eps5 gene; Eps5 gene; Eps5 gene; Eps5 gene; Eps5 gene; Eps5 gene; Eps8 protein; eps8 gene; Eps8 protein; eps8 gene; Eps8 protein; eps8 gene; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pluvinet, A., Charron-Bourgoin, F., Morel, C. and Decaris, B. Implication of horizontal transfers in the chimeric structure of the eps locus of Streptococcus thermophilus IP6757
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Streptococcus thermophilus
Bacteria, Pirmicutes; Lactobacillales; Streptococcaceae;
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/transl_table=11
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/db_xref="G1:18076390"
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TITIAACTCCAATTACTACAAACATAGCCATATCTTTCTAAAGCGCATGTTGGATATCTT
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EQFYPCYFPTNRNFKNLVKNTFLALKILRKERPDVIISSGAAVAVPFFYLGKLFGAKT
VYIEVFDRIDKPTVTGKLVYPVTDKFIVQMEEMKTVYPKAINIGSIF"
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HQLDPAYQVKDRYDNIEVVEDIKTLQQFLKQDLSISESTTSNNKKFNEQLRQEVENIM
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Xolkman,M.A., van der Zeijst,B.A. and Nuijten,P.J. Functional analysis of glycosyltransferases encoded by the capsular polysaccharide biosynthesis locus of Streptococcus pneumoniae
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                               Kolkman,M.A., Morrison,D.A., Van Der Zeijst,B.A. and Nuijten,P.J. The capsule polysaccharide synthesis locus of streptococcus pneumoniae serotype 14: Identification of the glycosyl transferase
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Submitted (23-APR-1996) M.A.B. Kolkman, Institute of Infectious
Diseases and, Immunology, Department of Bacteriology, School of
Veterinary Medicine, University of Utrecht, P.O. Box 80.165, NL
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Submitted (16-JUN-1997) M.A.B. Kolkman, Institute of Infectious
Submitted and, Immunology, Department of Bacteriology, School of
Veterinary Medicine, University of Utrecht, P.O. Box 80.165, NL
-3508 TD Utrecht, NETHERLANDS
On Jun 17, 1997 this sequence version replaced gi:1279732.
Location/Qualifiers
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J. Biol. Chem. 272 (31), 19502-19508 (1997)
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                                                                                                                                                                      J. Bacteriol. 178 (13), 3736-3741 (1996)
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7 (bases 1 to 14943)
Kolkman,M.A.B.
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5 (bases 1 to 1821)
Kolkman, M.A.B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8828 ATGGGAGCAATTGCTAAAGGAAAAAACCGATTGTTGTTCCAAGACAGGAAAAGTTTGGA 8887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cps14E gene;
cps14J gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8888 GAGCATGTAAATGATCACCAATTAGATTTGCCTATCAAGTTAAAGATAGGTACGATAAT
       AGCTTTCAAAATTTTACGTGATGAAACCAGATGTTATTATTTTCATCTGGTGCGGCCGT
                                      1634 IGCTGTCCCCTTCTTTACATCGGAAAACTATTTGGAGCAAAGACGATTATATTTGAAGT
                                                                                                                                                                                    cosida gene; cosida gene; cps14C gene; cps14D gene; cps14E cps14F gene; cps14G gene; cps14G gene; cps14G gene; cps14G gene; cps14C gene; cps14E gene
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Streptococcus preumoniae
Streptococcus Lactobacillales; Streptococcaceae;
Bacteria, Firmicutem, Lactobacillales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9127 AATTACATCAAGTGTTÄTTTCTATGAÄGTTTTAAGTÄTÄTÄ 9167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ss-1,4-galactosyltransferase; tasA gene
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X85787
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                                                                                                                                                                                                     8408
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                                                                   8348
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ACCESSION
VERSION
KEYWORDS
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SPCPS14E
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KPEEFFSTTRIYVVRDQGEKGGLTNQDLQAGSYLVKDYREIILSQYVLEBVVSDLKLD
LTFKGLANKT KYTVPVDTRIVSVSVNDRVPEEASRIANSLREVAAQKIISITRVSDVT
TLEBARPAISPSSPNIKRNTLIGFLAGVSGTSVIVFLLEFLNTRVKRPEDIENTLQMT
LLGVVPNLSKLK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /trānslation="MPTLEIAQKKLEFIKKAEEYYNALCTNIOLSGDKLKVISVTSVN
PGEGKTTTSVNIARSFARAGYKTLLIDGDTRNSVISGVFKSREKITGLTEFLSGTADL
SYGLCDTNIENLFVVQSGPVSPNPTALLQSKNFNDMIETLRKYFDYIIVDTPPVGIVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DAVIITQKCDASILVTATGEANKRDVQKAKQQLEQTGKLFLGVVLNKLDISVDKYGVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5035 TGGCAGTATTACAGAGTATTATTGTCATTTTATTGCTTTATTTCTTAGCTTTGTTAGAG 5094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5275 AACGGTTTAGTATCTCTAGAAGAATGGTATACTTCTTAACTTTAGAAGGAATATCCT 5334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5395 ATAGCAAGAAATTTTACTGTTAACAGTAACGGAAAATATAGAAAAGTTCTTGATAAAT 5454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5007. .6374
gene="cgp14E"
/function="capsular polysaccharide synthesis"
/note="homologous to Cps19fE ofS. pneumoniae serotype 19F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           316 TATACCTATTTAACGTAATTATTAAGCAGTTTAAGGATAGCTTTCTATTTTCGACAATCT 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5215 CTATAAGATATATTTTTTTTTTTGCAATAGCTATAAGTGTATTAAACTTTTTTATAGCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5335 TATACTTGTTAAATTTCTTAGTAAAGAAATATTGGAAGCATGTGTTTTTAATCCAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              376 ATCAAAAAAAGACGATTCTAATTACAACGGCTGAACGATGGGAAAATATGCAAGTTTTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATGCTGATTTAAATCGTTCTGGAATTTTTATCATAATGATGGTTCATTATTTTGCATTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              136 TTATATCTCGTATGCCAGTTGAATTTGAGTATAGAGGTAATCTGATAGAGTTTGAAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   196 CATTTAACTATAGTATAATATTTGCAATTTTTCTTACGGCAGTATCATTTTTGTTGGAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        256 ATAATTTCGCACTTTCAAGACGTGGTGCCGTGTATTTCACATTAATAAACTTCGTTTTTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGGCATTATTTGATATGATAGCAGTTGCAATTTCTGCAATCTTAACAAGTCATATACCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="capsular polysaccharide synthesis protien"
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/db_xref="UniProt/TrEMBL:P72512"
                                                                                                                                                                                                                                                                                                                                                                          function="putative polysaccharide export protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21;
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Pred. No. 4.9e-91;
0; Mismatches 859;
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4308. .4991
                                                                                                                                                                                                                      gene="cps14D"
                                                                                                                                                                                                                                                                                                       gene="cps14D"
                                                                                                                                                                                                                                                                                                                                                                                                codon start=1
transl table=
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/gene="cps14E"
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5007. .6374
                                                                                                                                                                                                                                                                                                                                                    gene="cps14D"
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62.7%;
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Best Local Similarity 62.77
Matches 1482, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4.SYGNYGKK
                                                                                                                                                                                                                                                                                                                               4308.
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| db xref="UniProt/TrEMBL:007338" |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LNATSNYSEYSISVAVLADSDIENVTQLTSVTAPTGTDNENIQKLLADIKSSQNTDLT
VDQSSSYLAAYKSLIAGETKAIVLNSVFENIIESEYPDYASKIKKIYTKGFTKKVGAP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KGMFETPEEKIAENFLQVREIAKEVADDLVIAYGAEIYYTLDALEKLEKKEIFTLNDS
SYALLIEKSMFTSYROLHTGLANILMLGITPVIAHIERYDALENNEKHYRELIDMGCYT
QINSYHVSKPKFFGEKYKFKKKKRAYFLERDLVHVVASDMHNLDSRPPYMQQAYDIIA
KKYWSQKSERTFVDNPRKIIMDQLI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'db_xref="UniProt/TrEMBL:P72510"
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EFSALHGKFHPPVGNYHLDSEQALGFYRERYSLADGDRDRGRNQQKVIVAILQKLTST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EALKNYSTIIDSLQDSIQTNMPLETMINLVNTQLESGGNYKVNSQDLKGTGRTDLPSY
AMPDSNLYYMEIDDSSLAVVKAAIQDVMEGR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'trans1_table=11
product="capsular polysaccharide synthesis protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              function="putative chain length regulator"
                                                                                                                                                                          .10552,10568. .11416)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                function="putative regulatory"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        table=11
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419. .2864
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                                                                                                                                                                                                gene="cps14K"
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408. .1410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene="cps14A"
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trans1 table=
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transl_table=
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                                                                                                                                                                                                                                                                                     .1365
                                                                                                                                                     700. .753
join(1054.
                                                                                                                                                                                                                                                                                   360.
                                                                                                                                                                                                                                                            repeat_region
-35_signal
                                                                                                                                                     terminator
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1576	233 TAACTITACAICAAATAATAATTTTTTTTTGTGAAAGATTAAAACAATAGTTGAAAA 228 233 TAACTITACAICAAATAATAATTATTTTTTTTGTGAAAGATTAAAACAATAGTTGAAAA 228 2290 ATTTAATGAGAATAACAAAATAATAAAAAAAAGAAGATTTTGTTGATAATTGAATAAT	RESULT 7 A1376403 LOCUS LOCUS LOCUS DEFINITION Streptococcus agalactiae strain 7271 Cps7C, Cps7D, Cps7F, Cps7G, Cps7H, NeuB, NeuC, NeuD, and NeuA genes, complete cds. ACCESSION A7376403 RESPONDED A7376403 A776403 A77
136 TIGAMICACATAAACAAATTCAAAAAATTCTGTGGATTTTTGGTAGTACAGAAATTCTGTGATTTTTGGATAAATTTTGTGATAAATTCTGTGAAACTGGTAGCGTAGTTTTTTTT	6103 GGÀÀIGICTITÀIAGAGÀIÀIGÀGITIGAGAGAGACACCTAIAGACAGAGI 6162 1156 TIGAAAAATATACTCCTGGTCAAAGAGACGATTGAGTTTAAACCAGGGATTACAGGTC 1215	

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                                                                                                                                                           /note="capsular polysaccharide repeat unit polymerase"
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                         Cieslewicz, M.J., Glusman, G., Chaffin, D., Kasper, D., Madan, A., Acdrigues, S., Fahey, J., Wessels, M.R. and Rubens, C.B.
Evolution of group B Streptococcus capsular polysaccharides
Unpublished
2 (bases) to 14202)
2 (bases) to 14202)
Cieslewicz, M.J., Madan, A., Wessels, M.R., Kasper, D. and Glusman, G. Direct Submission
Direct Submission
Submitted (28-Ad06-2003) Channing Laboratory, Brigham and Women's Hospital, 181 Longwood Ave, Boston, MA 02115, USA
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/note="capsular polysaccharide chain length regulator"
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CACGAGATACCAAAGTTGTTTTGATAACGAATAAGGATTCTTTATCAAAAATGACCTTTA 1995
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                                                                                                                                                                    ATTGTTATGATTTGAAACATAACTCGTTAAGGATAATAAACAAAGATGCTCTTACTTCAG
                                                                                                                                                                                                        TTTCAACAAGGGAAGTGGTCGACCACGTCTTTATAAATCTACCAAGTGAGTTTTTAGACG
                                                                                                                                                                                                                                           AGITAACCTGCTTAACTGTTGATCAAGCTTTTATTAACATACCATTGAATTATTTGGTA
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                                                                                                                                                                                                                                                                                                                                                                                          ATGTAGAGGCACTTAGCTTTGATAATATAGGAGAAAAGCGAATCCAAACTTTTGAAGGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note="UDP-N-acetylglucosamine-2-epimerase"
                                                                                                                                                                                                                                           synthetase'
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Pred. No. 7.3e-86;
                                                                                                                                                                                                                                           'note="N-acetylneuraminic acid
                                                                                                                                                                                                                                                                                              /product="NeuB"
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                 /protein_id="AAR25955.1"
/db_xref="GI:38640644"
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/transl_table=:
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CCTGTTTGATAATAGCTACTCTATGTTA--TTGA 4742 AATATTAGTTAGTTTTTGGGAAAATATTTT 4922 PATATTATTCAAAATGGGAAAGATATTGTATTTTT 3457 sgaacgaacgraarrargargrraccaaaaararr 5162 CAATITITITICITGIGCTIGCTITITATACCGAI 3637 GATTTTGTGCCAATTCTTTTATCAAATGAAAACG 2743 AACATTAAATTATTTACTGTATCAATATACTTTT 4444 ICCTATTGTCTTTACAGATGATTCTATTGATGAAT 2917 rcartracactreragaceerrreacterrrr 4684 TTTTTATTTATTTTATGAATTTAATTTTATTTCA 3157 VIATTAAAAAATGAAATTTTATTTATTATG 3217 STCACAAGTATGTTGTTGAAATAAATTTGAAAG 3277 ACTGCTATITATAATGTCTATAGTATTATTTACAG 4862 ATAATTTGGATTATTGCAATAATGTATTATAATTT 3337 ACAAATGATACCTAAAGTTATACATTATTGTTGG 5042 PATCTTATAACAGGCGTCAAAACAAGGTTGGTTGG 3517 ATTTAAAAAGTACATAAAACCTGGAGAGAACAA 5102 ACCACTACAATTATAGTTTCAATTCCGTTAATCTT 3577 SAATTITATTAAGAATGTATCGAGCTTTTGAATAC 2623 ATAGAATAAAAACATGGTCTAAGAATAAGATTTG 2683 PAATGTCCAGATGAACTATTTATACAGACAATTA 2803 TTTTTTTGTATTGTACTCAATTATAAACGACTG 4384 ATTATCTAAATATGGAAATTTAAGA-----TATA 2857 ITTATTTGCTAGAAGTTAAAAATAGAAATAAAT 2977 AAAATAAAATAGTTGATTTTTGTGAGAGTAATGTAT 3037 SAATATTTTTATTTTAAGTACTTCTGGTTGATTAT 3097 aagciricicraraaraagarcgcgrararg 4204 GAAATTAGATTTTGTAGAAATAAAGTATGTCAAT 4264 APTTAGCACCATATACAGTTTTTTTTTTTAGCA 4564 rttrcaartrtrgricaaaartagataag 4624

	4776 AACACGTG	 6357 AATTGCGT	4836 GCTTATTA	6417 GCAGTCAT	4895 ACCCCTTT		4355 AGGILMAN 6537 TGGAGGAA	5015 TATTAGAG				5135 IGITATAT 6710 TCTTAAGA	5194 TTCCAGTT		5254 ATTATAAA		5314 TATGCAAG	6890 ICIGIGAC	6950 GCTTATCT	5434 TTGACTCT	 	5494 AAAGTAGA 		5554 TTGAAGTG 			5674 ATAAGAAA	7247 ATAAGAGA	5734 TTTTAAT 	5794 ATTTTAT	=======================================
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3638 CTATTTAAGTGGATCGAGAATTGGTAGTTTATCGCTAGCAATATTAATTA		3698 ATGGAGATATATAGGTGGAAAATTTGCTTGGATAAAAAGGTAATAGTAATATTTGTAAT 3757 c. 28.3 mmaga.comminga.ca.com.ca.a.a.a.a.a.a.a.a.a.a.a.a.a.a.a.a.a.a	ACTACTTATTATATATACTGATTGCTTTACCATGAAATTTTGGCTGTTAAAT				3876 TTAGAAAACAATATTTATTTGGATATGGAATATCGGAATATTCAGTTACGGGAACTTGG 3935	5463 CTTTTAAAAAAGGACTGAAAAGTAAAAATATCATACAAGTTATTGATGGTGTCACTATT 5522	3936 CTCGGAAGTCATTCAGGCTATATATCATTTTTTTATAAATCAGAATAGTTGGGTTGATT 3995	TTACTGATGTTTTTTTTTTTTATATAAAAAAAGTTATGGAGGAAACA		GCACTATTTTATTTTACATCATTAGCCATATTTTTCATATATAAACAATAGATCCGATT	11CCIGALICGAIGAAAALIA-GAGIAAGACIIGIAALIIGALIITAIALIIGGAIALGGA	ATIATITATATITAGIACTATITCITITATICATAGGIATITGGAAIAATATAAAAAA	555/ ACAIAIAGAAKGGCIGIIGCGIIIIIIAAAGCIIAAGACAGIAGICGCIAIIAACIGAAAAIA 5/55 4176 AAGGATATGGAGACAAAAAATGAATGATTTAATTTTCAGTTATTGTACCAATTTATAATGT 4235		4236 CCAAGATTATCTTGATAAATGTATTAACAGTATTAACCAAACATATACTAATTTAGA 4295	5817 GGCACCTTACATCGAAGAAACATTAGAAAGTGTCATGGCCACAACTTATTCAAATCTAGG 5876		AAATATTAATTGTTGTGATGGCTCAACTGATTACACATCAGTTATATGCCAAAAATACAC	4356 GAAGAACCATGGAAGAATTAAATATTAAATTAATGGCGGTCTAGCAGATGCTCG 4415 	AAATTTCGGACTAGAACATGCAACAGGTAAATATATTGCTTTTGTCGATTCTGATGACTA		4476 TATAGAAGTTGCAATGTTCGAGAGAATGCATGATAATATAACTGAGTATAATGCCGGTAT 4535	6057 CTGCTCACATTCTATATAGAATATTTAGTAAGAGTGCAGAGTGAAACTGGTGCTGATTT 6116	4536 AGCAGAGATAGATTTTGTTTAGTAGACGAAAACGGGTATACAAAGAAAAAAAA		GTCAACTTACTCAACACTCAGTGTGGAAAGCGACATTAACAGAAATGTACTATGATAACTA	4656 AGABAATAATGCTGCAAGCTTTATTCACGAGATATTATAAAAGATATAAAATTCCA 4715	6237 CGGTATTTCTCCATTGGGAAAGTTATACTCTAAAGCATTATTAAGACATCCATACC 6296	4716 AATTAATAATAGAAGTATTGGTGAGGATTTGCTTTTTAATTTGGAGGTCTTGAACAATGT 4775
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TTTAGCAAAGAGAAAACAGTATATATAAAAGGTCAACCTAATAGTACGACTAG 6416 GGAATATGCAGAAAAAGATAAAAGAGTAAAAATTTTTTCACTAATCATAGTG 5373 AAATGCTAGAAATCATGGAATAAAGCGGAGTACAGCTGAATATATTATGTTTG 5433 GAATAATCCAAATATTGAATTTTGAAGCAATTAATACCGTGCAGGACATGGGAG 5613 TATTGTTTTAGAGAATGAAGAATAGAAACAATTAGTCCGCTACAAGCAATAC 7186 TTTTATGAATTTGTATATAATAATATTTTTTTTTCTACTCCTGTTTGTAAACTAT 5673 TTATAATTATGATGACTATAAAGCTATTTTACTGTAGCACATAATAAATTAT 7246 AAGATACATAACAGATCTTTTCAAGAGAATCAATGGTTAGGAGAAGATTTAC 5733 agaattattttctacaatgigitacccagtaggaaactacacgaagatgaat 7306 GTAGTAGTTGATACTAGAGAATATTATTATTATTATGTCATTCGTAACAGTTC 4835 GAACGITATICAGACAAAGAACTAATCGATGCTTTAAATTATAAAACTGTAAT 6536 ATGITTAAACAAAATGTATTCAACAGATTGTTTGGATAATGAGTTCTTGCCAA 5014 AIGIGGATCGTTAATAAGCTTCTAGAAGTTGATAAATACGATTATAATTC 6596 AGTGAATATAGAAAATATTACAAGA-----GTATATTTATTTAATAAAGGTG 6649 TAAGAAATTTCAAAAGCAGTAGAGGTAAA-AATGGATAAAATTAGTGTTATTG 5193 TTATAATGTAGATAAATATTTAAGTAGTTGTATAGAAAGCATTATTAATCAAA 5253 Tracaargiicaarciiticiaaargaargiatagaragigiitiggcicaaa 6829 AAATATAGAAATATTATTGATAGATGATGGCTCTGTAGATGATTCTGCTAAAA 5313 rgargartartara---raaagaagargcaartgaggaaarggriggargra 7066 ATATGATTCAGATATTGTTTTAGCATGTTATGTTGAAAGAATAGGACAACGAA 7126 TCTGCATTATTAAAGAATATAGATAGAGTTAGTTATTTGACTGAACATCTTT 5793 AATCAGAAATTCTCTATAAATAATATTGATTTAGT-CACAAGATTGGAGAATT 4894 PARGTTAAAAAGAGAGTTTAGTCATTATTTTGATGCAAAAGTTATTAAAGAGA 4954 AAAGCATTTAGTTTACGTTGTATTTGATGAAATTTTCGCCTAAACTATATGTAA 5134 AAAAGAAAAATAAAATATCTGTCATTTATTTCCTCAATGAACCTGTTTTTAT 6709 AAGTGATTTATCTGGTTGTTTGTACGCTACTTTTTCAGAAAATATAAATAT 5553 GTCTTATCGAAAAGAAATACGTAGATATCCATTTATTAAAGCGAAAAGATATT TAGGAGAGGTATACTAGTACAGTAAATTCTTTTAAAGAAGGT 5843

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KELDSLYFERRKLVIFLLETATILLAFPKHVYPFILTLIPFLAKUNDISLKKAFSII
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VLPVQFFLLVYTPKSSTIFRNSNPFVQKLDVLLTGRLHYAHLQLVDGITPFGNSFKETS
VLPNSSYSMLLSMYGVVLTMFCMIIYYIVSKKIIIIBLQLLLFIMSIILFTSFFYBSV
VMNISWLLSMYGVYLTMFCMIIYYIVSKKIIIIBLQLLLFIMSIILFTSFFYBSV
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DVSKNVFWREAXTKKNFAYSDYARLDIIYTYGGFYLDTDVELLKSLDPLRIHGCFLA
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IIGKLDDIITYPRNYFPRPKNLLIGKVDCLTSVTYSIHHYBGSWKSSEFISDSLKIRVR
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                                                                                    note="beta-1,4-galactosyltransferase"
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codon start=1
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|codon_start=1
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Pred. No. 2.6e-81;
0; Mismatches 3382;
                                                                                                                                                     protein_id="AAK29653.1"
db_xref="GI:13549131"
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db_xref="GI:13549132"
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| gene="cpsVN"
| 8762. .9649
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/gene="cpsVM"
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/gene="cpsVM"
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                                 AAAAATTTTATGAATTTGTATATAATAATATTTTTTTCTACTCCTGTTTGTAAACTATAT
                                                                                                     AAGAAAAGATACATAACAGATCTTTTTCAAGAGAATCAATGGTTAGGAGAAGATTTACTT
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I (bases 1 to 21365)

Tettelin,H., Masignani,V., Cieslewicz,M.J., Eisen,J.A.,

Peterson,S., Wessels,M.R., Paulsen,I.T., Nelson,K.E., Margarit,I.,

Read,T.D., Madoff,L.C., Wolf,A.M., Beanan,M.J., Brinkac,L.N.,

Madupu,R., Lewis,M.R., Radune,D., Fedorova,N.B., Scanlan,D.,

Khouri,H., Mulligan,S., Carty,H.A., Cline,R.T., Gill,J.,

Scarselli,M., Mora,M., Iacobini,E.T., Brettoni,C., Galli,G.,

Mariani,M., Vegni,P., Malone,D., Rinaudo,D., Rappuoli,R.,

Telford,J.L., Kasper,D.L., Grandi,G. and Fraser,C.M.

Complete genome sequence and comparative genomic analysis of an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tettelin,H., Masignani,V., Cieslewicz,M.J., Bisen,J.A., Pettelin,H., Masignani,V., Cieslewicz,M.J., Bisen,J.A., Pattelin,H., Masignani,V., Paulsen,I.T., Nelson,K.B., Margarit,I., Read,T.D., Madoff,L.C., Wolf,A.M., Beanan,M.J., Brinkac,L.M., Daugherty,S.C., DeBoy,R.T., Durkin,S., Kolonay,J.F., Umayam,L.A., Madupu,R., Lewis,M.R., Raddune,D., Fedorova,N.B., Scanlan,D., Khouri,H., Mulligan,S., Carty,H.A., Cline,R.T., Gill,J., Scarselli,M., Mora,M., lacobini,E.T., Brettoni,C., Galli,G., Mariani,M., Vegni,F., Malone,D., Rinaudo,D., Rappuoli,R., Telford,J.L., Kasper,D.L., Grandi,G. and Fraser,C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genomic Research, 9712
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         emerging human pathogen, serotype V Streptococcus agalactiae Proc. Natl. Acad. Sci. U.S.A. 99 (19), 12391-12396 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="identified by match to PFAM protein family
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptococcus agalactiae 2603V/R
Streptococcus agalactiae 2603V/R
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Streptococcus agalactiae 2603V/R"
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                                                                                                                                                                                                                                                 complement (5389. .6276)
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Best Local Similarity
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10.	10105 CACGAGÁTÁCCAÁAAGTTGTTTTGÁTAAÓGÁATAAGGÁTTCTTTATCÁAAAÁTGACCTTTA 10046	ò	1487 AAGA
-	433 TATTTGAATCACATAAACAAATTCAAAAAAATCTTGTTGCATTGGTAGTTTTAGGTACAG 492	같음	
10	10045 GGAAȚAÀȚACGACATAAȚTATATCGCTGTCTGTATCTTGGATTCCTCTGAAAGG 9989	ð	
-	493 AAATAGATAAAATTAATTTATCATTACGCTCTATTATTCTGTGGAAGAAGCTATAGAGT 552	r 8	
6	9988 ATTCTTATGATTTGAAACATAACTCGTTAAGGATAATAAACAAAGATGCTCTTACTTCAG 9929	è	
	553 TITCAACAAGGGAAGTGGTCGACCACGTCTITATAAAICTACCAAGTGGGTTTTTAGACG 612	3 f	
6	9928 agiraactgritaardardargcritiarraacaraccartgaarrarirggra 9869	ł è	1667 TGGAC
	613 TAAAGCAATTCGTITCAGATTTTGAGTTGTTAGGTATTGATGTAAAGCGTTG 663	3 8	
6	9868 AATACCAAATACAAGATATTATTATGACATTGAGCAATGGGAGTGATTGTCAATGTTA 9809	ìè	1727 AAAA
	664 ATATTAATTCGGTTTTTACTGCGTTGAAAAAAAAAAAAA	डे ह	
ο̈́	9808 AIGTAGAGGCACTTAGCTTTGATAATATAGGAGAAAAGCGAATCCAAACTTTTGAAGGAT 9749	i è	787 ATATA
	724 ATAGCATTGTAACTTTTTCCACAAATTTTTATAAGCCTAGTCATATCATGATGAAGGAC 783	3 6	111
6	9748 ATAGTGTTATTACATATTCTATGAAATTCTATAAATATAGTCACCTTATAGCAAAACGAT 9689	3 8	2042 7841
	784 TITIGGATATACTCGGAGCGGTAGTCGGGTTAATTATTTGTGGTATAGTTTCTATTTTGT 843	S	
ō	9688 TTTTGGATATCACGGGGGCTATTATAGGTTTGCCCATATGTGGCATTGTGGCAATTTTC 9629	3 8	A 1001
	844 TAGTTCCAATTATTCGTAGAGATGGTGGACCGGCTATTTTTGCTCAGAAACGAGTTGGAC 903	ਤੇ ਵੰ	1907 AIAM
6 qa	9628 TAGTICCACAAATCAGAAAAGAIGGGGGGGGGGTATCTTTTCTCAAAATAGAGTAGGTC 9569	i è	24F4F 5301
λ	904 AGAATGGACGCATATTTACATTCTACAAGTTTTCGATCGA	S	
0	9568 GTAATGGTAGGATTTTTAGATTCTATAAATTCAGATCAATGCGAGTAGATGCAGAAAA 9509	à à	
	964 GCAAAAAAGACTTGCTCAGCCAAAACCAGATGCAAGGGTGGGT	3 5	8434 ATCAC
6	9508 TTAAGAAAGATTTATTAGTTCACAATCAAATGACAGGGCTAATGTTTAAGTTAGA 9454	}	2087 1716717
	1024 AAACGAICCTAGAATTACTCCAATTGGACATTTCATACGCAAAAACAAGTTTAGACGAGT 1083	S &	8374 6466
Ó	9453 CGATGATTCTTAGAATTAATTAAAATTAGGAAAATTTATTT	3	

8975 1546 1606 1666 1726 1786 1846 8495 2026 8435 9275 8855 8795 TGCGACGGAGCCCCGCTACTTTATGAATTCATTATCCAAAGGAAAAAACAATTA 2086 TITICCTAGACAAAAAAGTATGGTGAACATGTAAATGATCATCAAGTAGAGTTTGTA 2146 ----ATGAAAGTTTGTTTGGTCGGTTCTTCAGGGGACATTTGACTCACTTGTATT 1426 BACAGCAGTTCAACCGTCTTATTAAAGAAGTTGATAGATAAAAAGGGACAGGGTGCT 8555 ACCGACGAAATATTTATTCAAACAGGATATTCTGACTATATTCCAGAATATTGCAAG 1966 SGTTGGACTTAGCATTGATAATTGGACTATCTGGTCAGATATTAAATTTTAT 1323 TATTATTTCATCTGGTGCGCCGTTGCTGTCCCCTTCTTTTACATCGGAAAACTATT NAAACCGTTTTGGAAGGAAGAAGAACGTTTTTGGGTAACATTTGATAAAGAGATGC AGCAAAGACGATITIATATIGAAGTATITIGATCGAGTIAATAAATCTACATIAACTGG PTACAGGTCTCTGGCAGGTTAGTGGTCGTAGTAATATCACAGACTTCGACGACGTAG

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6234 TTATCCTATC-TGTATGATTCTCTATGTAATCAGACAAATAAAAATTTATATGGTTGAT 6176 4356 GAAGAACGATGGAAGAATTAACAAGAAATTTAATGGCGTCTAGCAGATGCTCG 4415 6175 TGTTGATGGTCTGAGGACTGTACTAGCAGAAATTGTAAGTAA	4536 AGCAGAGATAGATTTTGTTTAGTAGACGAGATACAAAAAAAA	### ##################################			TATAAAATÄTAGAAATATTATTGATAGATGGCTCTGTAGATGATTCTGCTAAAATA

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5915 6095 4468 6155 6215 6275 6335 6395 4767 4359 5495 5002 5675 4941 ATGTATTATGGGAAAACTTATGGAGTTTCCCCGTTAGCAA----AATTATATCCGAGAA 4887 5735 5796 TITTATAGGAGAGGTATACTAAGTACAGTAAATTCTTTTAAAGAAGGTGTGTTTTTGCAA 5855 5916 GACGTATCAATTGTTAAAGATACTATACGTTGGCAAGTATTTTATTATAGCTTACTAATG 5975 5976 TTTAAATACGGAAAACAGTCTATTTTTGACAAATTTTTAATTTTTAGAAATCTTTAFAAA 6035 4587 GATTTTAAATTATATGATACAGTTGATTATTACAGAAAAAAATATAGAAAATATTTTAAG 4528 4358 AACGAGTGTATAGAAAGTGTTTTAGCTCAAACTTATTCAAATTTAGAAATTATTCTAGTT 4299 4298 AACGATGGCTCTACAGATAATTCCGGGGATATCTGTGATTATTATTCAGAAATAGATGGG 4239 4238 cGTATATTCGTTTTTCACAAAATAATGGTGGTTTATCAGATGCTCGTAATTATGGAATT 4179 4118 GATGCAATCGAGAGAATGGTTGAATTTAGCGAGAAATATAATTCAGAAATTGTTTTAGGG 4059 GACTCTGATGATGTTGTTGGTAGTAGTAGAAAAATTATATTTTAATATATAAAA 5001 ATTAATTCACAGTATTTAAAAGAGATTAAACTTTATACTTTAGAGGTGGCGTTGGAAGAA 4886 GTAATTTATTGAGTAATCCATATCCAGAAGGAAAATTCATGAAGATATGGATACAACTT 4467 TCCTCTATAAGATATTTCACTATTGTAAGAAAATA-----TATAATTTGAGGTTATC 6156 ATGGATACTATTAGTAAAATTTCTATAATTGTACCTATATAAATGTAGAAAAATTTTA 4414 AAGGA----AIGGAIAAAGIIAGIAICAIIAICCOOTIIAIAACGIICAAICTIICCIA 6216 TCTAAATGTATAGATAGCATTGTAAATCAGACCTACAAACATATAGAGATTCTTCTGGTG 6456 TT----CATCCAACGTTTACACGAAGCAATTGAGAGAGAGAATGCCCTTGTGGCAGTTGCT 5121 GACAGTGATGATTTTATTCAATTGAGGTTATGTACAACATACAGAAGCT 5676 AAGAAAAGATACATAACAGATCTTTTCAAGAGAATCAATGGTTAGGAGAAGATTTACTT 4826 Traagcriararicrigggcricaaaaraggggringrgararicrcacrgcagrggrgr 5856 TTGGAAAATTTGCAAAAACAAGTGATAGTATTGTTTAAGCAAATATATGGTGAGGATTTT 4707 GAGGCAATICAAAATAATATTGTATTTATAAATCTAAATTTTCCACATAATACATCTTTA 4527 ACTATICTCITITAATAAGATTAGTGTGAAGGAGAGGTTAAATATATTATTTATT CGCATTCGTTATTTAAAAAAAAAAACGCCGGCCTATCAGATGCCCGTAATTATGGCATA 5061 Accaargccdaratrorirraacragrarrograacrircaacaaracraaracragr GAAGTGAATAATCCAAATATTGATTTTGAAGCAATTAATACCGTGCAGGACATGGGAGAA 6036 AAATATTTTTAACTTGTTAAAAGTATCTAACAAAAATTCTTTGTCTAAAAATTTTTGT 6096 ATAAGAATTGTTTCGAACAAAGTTTTTAAAAAAAATATTATATAATAGGAAGATATC 5496 AGTAGAAGTGATTTATCTGGTTGTTTGTACGCTACTTTTTCAGAAAATATAAATTTT 5436 6336

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GAATCACTGGTTTGTGGCAAATATCTGGTAGAAATAATATTATTACTGATTTTTGATGAAATCG 245985
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TGGTATTGAAATACAGCTTTTACTATATTTTCATATCAAGTTCATTATTTTTTATTTTTA
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                                                       TGTTATGTTGAAAAAAGAACAACATATTATAAATATCGTTTTAGAAGATGAAATGATA 3999
                                                                                                                                                            GAAACTATTAGTCCAGTACAAGCAATACAAAATATTATAA---TTATGATGCCTATAGA 3942
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() Organism="Streptococcus agalactiae"

//organism="Streptococcus agalactiae"

//mol_type="unassigned DNA"

//db_xref="reaxon:131"

//noTe="seq 10967 to big: splitted in-seq 10.967, from 0.000 to 0.149.980-seq 12.025, from 0.300.001 to 0.649.980-seq 12.026, from 0.500.001 to 0.949.980-seq 12.027 from 0.900.001 to 1.249.980-seq 12.028, from 1.200.001 to 1.249.980-seq 12.029, from 1.800.001 to 2.149.980-seq 12.031, from 1.800.001 to 2.149.980-seq 12.031, from 2.100.001 to 2.160.266"
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                                                                                                              ACAAATCAGGCTGTTCTGAGCGGCAGGAATGTTTGTAAAAAGCTGCTAGAGGCGGATGGT
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Nucleic acids and proteins from streptococcus groups a & Patent: WO 0234771-A 12027 02-MAY-2002;
Chiron S.P.A. (IT); THE INSTITUTE FOR GENOMIC RESEARCH Location/Qualifiers
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TAAAGTTAGATGTTCA	TAAAGACAGTGAAAGT	 	ATGAAAGTT GAATATAATGAAAATT	GTTAAAACCGTTTTGG TTTGAACCCATTTGG	AAGAAGTCTTTTGAAG	TAGGAGTATTCTAAGA	CAAAAACTTGGTAAAA	TGTTATTATTCATCT TGTTATCATATCATCT	TGGAGCAAAGACGATT	AAAACTAGTTTATCCC	 AAAATTAGTGTATCCT	ATATCCTAAATCTATT TTATCCTAAGGCAATT	CATGAACAACAGTTTA		ataaccgacgaaatat 	TATAAAAATTTCTCA	rggrcaaaarrrcrcr	ATTTGCCACGGAGGCC 	TTGTTTCCTAGACAAA	GIGGIICCIAGACAAG	AGAAGAATTTTACAAG 	AAAATTATTGAAGTTT		GAAAGATTAAAACAAA GAAGAATTTAAGGTAA	AGATGCATATTTGATA	TTATATTGCAATATTT
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                                                       241656 GTAATTTATTGAGTAATCCATATCCAGAAGGAAAATTCATGAAGATATGGATACAACTT
                                                                                        241596 TTAAGCTTATATCTTGCGCTTCAAAATAGCAGTTTGTGATATTGTCACTGCAGTGGTGT
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/mol_type="unassigned DNA"
/mol_type="unassigned DNA"
/mol_e="texon:314"
/note="seq 1373 to long, original length:
2.160.266~replaced by~seq 1373: from 0.000.001 to
0.349.980~seq 1374: from 0.300:001 to 0.649.980~seq 1375:
from 0.600.001 to 0.949.980~seq 1376: from 0.900.001 to
1.249.980~seq 1377: from 1.200.001 to 1.549.980~seq 1378:
from 1.500.001 to 1.849.980~seq 1379: from 1.800.001 to
2.149.980~seq 1380: from 2.100.001 to 2.160.266"
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Nucleic acids and proteins from streptococcus groups a b.

Patent: WO 03093306-A 1376 13-NOV-2003;

Chiron SRL (IT); THE INSTITUTE FOR GENOMIC RESEARCH (US)

Location/Qualifiers
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Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
Streptococcus.
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Pred. No. 9.7e-82;
0; Mismatches 3382;
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ABABABAGTATGGTGAACATGTAAATGATCATCAAGTAGAGTTTGTA 2146 MATGATGATCGTCCGTTTTTAGAACTAATAGTAGTAATTTTATT 273752 ATTATTTATCGCGACCATTTTGAATTTATTCT------- 273498 274112 273992 AATGTATAATTTTGATATCGTTGTAGATATTGAAAGGTTACAAAAT 273812 zariariaaaggagrigrgggargaaarcaaraaaagcrcrrrarr 273692 TTTTAGTTAATTTTTTTAATCACTGGGTTTAGGCGAGGGAAACTC 273632 TG-----ATGTTAGTTGCAA 273603 274352 2026 AAAATACTTTCTTAGCTTTCAAAATTTTACGTGATGAGAAACCAGA 1606 NTTAACTTGGGGAGTATTTTTAATGATTTTTGTAACAGTAGGAACT 1846 TAATCGATTGATAAAAGAGATTGATTTATTGAAAAAAAAGGAAGT 1906 ATTITATICAAACAGGATATICIGACTATATICCAGAATATIGCAAG 1966 AGATAATAATATTTTATAGAAAATATAGATGATTTGTTTGAA 2206 AATAGTTGAAAATTTTAATGAGGATCAAGAAAATGAATAATAAAAA 2323 TCTCTCAGGAGAATGCACCACTAGTTCCTTCAGAATACCTGTAT 2443 ATTCTCAGGATTTATATGTTGAATTTACAAAAGATGAGCAAAAATAT 2503 PATATGAACGAGTTAAATGTTACAGATTATTTCCTAATATATCAGAA 2563 CTGGTGCGGCCGTTGCTGTCCCCTTTTACATCGGAAAACTATT 1666 ATAATGGCTTATCATAATTTTTCTCAGATTTTTACTGGAGAGGGATAC 2383 ATGTACTGTTTAGAATTTTATTAAGAATGTATCGAGCTTTTGAATAC 2623 TITATATTTGAAGTATTTGATCGAGTTAATAAATCTACATTAACTGG CAGTTACAAAGAAATGGAACAATATATTAACAAATCAGAAGTAGTT TTCTAAGCAAACTAACTTTACATCAAATAATATT----TTTTTGT

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4776 AACACGTGTAGTTGATACTAGAGAATATTATATATTATGTCATTCGTAACAGTTC 4835 271323 TTCGAAGGGGACAATTCTTATCAGAAGAAATATGTATATATA	4836 GCTTATTAATCAGAAATTCTCTATAAATAATTAATTGATTTAGTCACAAGATTGGAGAATTA 4895	271263 TACTTTTGTCCCCAAAATAGGAAATCTATTGTTTTGACTACTTAGAAGATGGTTT 271208	4896 CCCCTITAAAAAAAAAAAAAAAAAAAAAATTATAATATTTGAAAAAA	271207 GACTICTAATATTTTAAATTATGGAGAAAAATTTCAAAGGGACTATTTTTTCATTAGA 271148	4956	271147	5016 ATTAGAGTCTTATCGAAAAGAAATACGTAGATATCCATTTATTAAAGCGAAAAGATATTT	Z/IUB9 AIAAAGAIAAAAAIGAACAIACAGCITICAAAAIGACIACITITAGGGGIAATACCIACA Z/I	50.06 ATCAAGAAGCATTTAGTTACGTTGTATTTGATCAAAATTTTCGCCTAAACTATTGTATT 5135 771070 CHRABAC	4.136 CTTERTOR BARATTER BARACTER CONTRACTOR BARACTER BARACTER BARACTER BARACTER CONTRACTER CONTRACTER CONTRACTER CONTRACTER BARACTER BARACTER BARACTER BARACTER BARACTER CONTRACTER CONTRACTER CONTRACTER CONTRACTER BARACTER BARACTER CONTRACTER CONTRACTER CONTRACTER CONTRACTER BARACTER CONTRACTER CO	270978 TGGAAGGTAGCAAGGTTTAAAAAGAGCGAGTAAAGAATGGAATTAATT	5196 CCAGITIAFAAFGTAGAFAAATATTTAAGTAGTTGTATAGAAAGCATTATTAATCAAAAT 5255	270918 CCTGTATATATAGAGAAATATATATTGGGAGATGTCTAGATAGTATTCTTGAGAAACT	5256 TATAAAATATAGAAATATTATTGATAGATGATGGCTCTGTAGATGATTCTGCTAAAATA 5315		5316 TGCAAGGAATATGCAGAAAAGATAAAAGGTAAAAATTTTTTTCACTAATCATAGTGGA 5375	270798 IGCGAAAAGIATITITIGGAAGACAGCGAATAAAATATITICTATCAAGAAAACAGGGGC 270739	5376 GTATCAAATGCTAGAAATCATGGAATAAAGCGGAGTACAGCTGAATATTATGTTTGTT	270738 CAATCAGTIGCACGIAACAACGGAGTACTIAGGIGTACAGGAGATIGGATIG	5436 GACTCTGATGATGTTGATAGATTAGTAGAAAAATTATATTTTAATATTAT	270678 GACAGTGATGATGATTATCTTCCTTATTCAATTGAGGTTATGTACAACATACAGAAGGT 270619	5496 AGTAGAAGTGATTTATCTGGTTGTTGTACGCTACTTTTTCAGAAAATATAAATATTT 5555	270618 ACCAATGCCGATATTGTTTAACTAGTATTGGTAACTTCAACAATACTTACAATACTTAGT 270559	5556 GAAGTGAATAATCCAAATATTGATTTTGAAGCAATTAATACCGTGCAGGACATGGGAGAA 5615	270558 ATTAATTCACAGTATTTAAAGAGATTAAACTTTATACTTTAGAGGTGGCGTTGGAGAA 270499	5616 AAAAAITITATGAAFITGTATATAATAATATTITTTTTTTTTT	270498 ATGTATTATGGGAAAACTTATGGAGTTTCCCCGTTAGCAAAATTATATCGGGAA 270444	5676 AAGAAAAGATAATAAGAGATCTTTTTCAAGAGAATCAATGGTTAGGAGAAGATTTACTT 5735	270443 GTAATTTATTGAGTAATCCATATCCAGAAGAAAATTCATGAAGATATGGATACAACTT 270384	5736 TITAAICIGCAITAITIAAAGAATAIAGAIAGAGITAGITATITIGACIGAACAICTITAT 5795	270383 TTAAGCTTATATCTTGCGCTTCAAAATAGCAGTTTGTGATATTGTCACTGCAGTGGTGT 270324	5796 TITTATAGGAGGGGATATACTAAGTACAGTAAATTCTTTTAAAGAAGGTGTGTTTTTGCAA	270323 AITITAGCGATAATAGIACTACTAGGACAAAAITCAATGAGAGAATGT-IGIAITITITI 270265 5856 ITGGAAAATITGCAAAAACAAGTGATAGTATTGITTAAGCAAATAIRGGGAGATTT 5915	
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270264 GAGGCAATTCAAAATAATATTGTATTTATAAATCTAAATTTTCCACATAATACATCTTTA 270205 270025 269915 AACGAGTGTATAGAAAGTGTTTTTAGCTCAAACTTATTCAAATTTAGAAATTATTCTAGTT 269856 269855 AACGATGGCTCTACAGATAATTCCGGGGATATCTGTGATTATTATTAGAAATAGATGGG 269796 269795 CGTATATTCGTTTTTCACAAAATAATGGTGGTTTATCAGATGCTCGTAATTATGGAATT 269736 269735 AGTAGAGCTACTGGCGATTATATTTATTTACTTGATTCGGATGATTATCTATATAAAAGAA 269676 269675 GATGCAATCGAGAATGGTTGAATTTAGCGAGAAATATAATTCAGAAATTGTTTAGGG 269616 269615 TGTTATGTTGAAAAAGAGACAACATATTATAAATATCGTTTTAGAAGATGAAATGATA 269556 269555 GAAACTATTAGTCCAGTACAAGCAATACAAAATATTTATAA---TTATGATGCCTATAGA 269499 269498 GCTATTTTTACTGTAGCACATAATTATATAAGAGAGAGATTATTTTTTTACGCTGTGC 269439 269438 TATCCAGTAGGGAAGTTACACGAAGATGAATTTTTAACCTATAAATTATATTTGAAAGCC 269379 269972 269971 AAGGA----ATGGATAAAGTTAGTATCATTATCCCAGTTTATAACGTTCAATCTTTCCTA 269916 6335 6395 6456 TT---CATCCAACGTTACACGAAGCAATTGAGAGAGAATGCCCTTGTGGCAGTTGCT 6512 5916 GACGTATCAATTGTTAAAGATACTATACGTTGGCAAGTATTTTATTATAGCTTACTAATG 5975 6513 GGTTATG-----ATAGGGTAGATGCTTCGGGGCATTTCTTAACAGCAGAGCCGCTTCCT 6566 6747 GAAAAAGTTGCAATAGTTAAGGAGTGCTTGTACTATTATGTTGACCGAGAAAATAGTATC 6806 5976 ITTAAATACGGAAAACAGTCTATTTTGACAAATTTTTAATTTTTAGAAATCTTTATAAA 6336 CGCATTCGTTATTTTAAAAAAGAGGCGGGCCTATCAGATGCCCGTAATTATGGCATA 6687 TITGAAAAGGGTAAGAITCAIGAAGAIGAATACTICACTITAICGCTIGCTCTAIGAGTIA 6036 AAATATTTTAAACTTGTTAAAAGTATCTAACAAAATTCTTTGTCTAAAAATTTTTGT 6096 ATAAGAATTGTTTCGAACAAAGTTTTTAAAAAAATATTATGGTTATAATAGGAAGATATC 270024 TCCTCTATAAGATATTTCACTATTGTAAGAAAAATA-----TATAATTTGAGGTTATC 6156 ATGGATACTATTAGTAAAATTTCTATAATTGTACCTATATAAATGTAGAAAAATATTTA 6216 TCTAAATGTATAGATAGCATTGTAAATCAGACCTACAAACATATAGAGATTCTTCTGGTG 6276 AATGACGGTAGTACGGATAATTCGGAAGAAATTTGTTTAGCATATGCGAAGAAGATAGT 6567 ACAAATCAGGCTGTTCTGAGCGGCAGGAATGTTTGTAAAAAGCTGCTAGAGGCGGATGGT 269318 ATGACTGGTTCCTACATATTAAAAGGCTACATGCTGTAGAAGCACTTAA 269269 6807 ACAACTTCTAGCATGACTGACCATCGCTTCCATTGCCTACTGGAATTTCA 6856

TION

AF355776 17596 bp DNA linear BCT 29-APR-2001 Streptococcus agalactiae CNTC 1/82 type IV capsular polysaccharide synthesis operon, complete sequence.

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                                                                                                                                                                     McKinnon, K., Chaffin, D.O. and Rubens, C.B.

McKinnon, K., Chaffin, D.O. and Rubens, C.B.

Direct Submission

Submitted (03-MAR-2001) Department of Infectious Disease,

Immunology and Rheumatchology, Children's Hospital and Regional

Medical Center, 4800 Sand Point Way NB, Seattle, WA 98105, USA

Location/Qualifiers
                                                                                              Streptococcus agalactiae
Bacteria, Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                    /organism="Streptococcus agalactiae"
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/db_xref="taxon:1311"
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/gene="cpsB"
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/gene="cpsB"
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                                                                              TATTATATATCTATTCATTTTTAAAATATTATCGAAAATATTCTTACGCTAAGTTTTT
                                                                                                             TCTATCAAAAAAGACGATTCTAATTACAACGGCTGAACGATGGGAAAATATGCAAGTTT
                                                                                                                                                                           TATITGAATCACATAAACAAATTCAAAAAATCTTGTTGCATTGGTAGTTTTAGGTACAG
                                                                                                                                                                                                          GGAATAAAT---ACGACCATAATTATATCGCTGTCTGTATCTTGGATTCCTCTGAAAAGG
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ESYPACELPGEVNTGLGFGSISRNPFIKENKIYEDTEYYSLKKTCVAITTDLLTEGG
LKYINKIQYINGILIYPPSYFCPVNMLTNKINIKEETLTIHHYGRNWGGEKKIIDLGR
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                                                                                                                                                      /translation="MXINKNSLFYIAIPLVNFFKSLGLGEGNSTYKIVMFVAIFLCGI
KFLLDSLYFERKLVIIFLLFIATILNLFFVHKVTFILTLIFFLALKDISLKKAFSII
IGSRILGVLLAQIFVKLDLIETKYINFYBOGOFILRSDLGFFGHNFFINFFRAVTFLY
VILFALTIAFILTLAFILTLAVYTYSTYQYTYSTOYYIVLFILIIYVTKNNLIRKIFMIV
APYIQLFLLAFFFLCSTIFFNSNFVQKLDSLLTGRLNFAHLQLVDGLTLFGNSFKETS
VLFDNSYSMLLSMYGVVLTMFCMIIYYIXSKKVNVVBLQILLFINSIVLFTESFFYPSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /protein id="AAK43611.1"
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/translation="MIEKTMIPKKIHYCWFGGNPKSELLLKCIKSWEKYCPDYEIIEW
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/transl_table=11
/product="putative_glycosyltransferase_CpsIVN"
                                                                                        /product="putative polysaccharide repeating
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/db_xref="GI:13876777"
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8931. .8936
/gene="cpsIVN"
8943. .9680
/gene="cpsIVN"
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/gene="cpsIVM"
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/gene="cpsIVM"
              /gene="cpsIVH"
6895. .7992
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/gene="cpsIVM"
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                                               'gene="cpsIVH"
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	1667 TGGAGCAAAGACGATTATATATAGAGTATTTGATCAGTTAAAATCTACATTAACTGG 1726 1	2027 AITTGCCACGGGGCCCCGCTACTTTATGAATTCATTATCCAAAGGAAAAAACTAT 2086 6621 ATCACACGGGGCCCCGCTACTTTATGAATTCATATCCAAGGAAAAAACTAT 6680 2087 TTGTTCCACGGGGCGTCCGGCGACGTTATGAATGCACTTCTAAAGGGAAAAAACTAT 6680 2087 TTGTTTCCTAGACAAAAAAAGTATGCGTGAAATGATCATCAAGGGAAAAAACTAT 6680 2147 AGAAGAATTTTCAAGAAAAATTTTATTATAAAAATATCTTGAAAGGTTACAAAAT 6800 2148 AAAATTATTGAAAAAAAATTTTATTATTATAAAAAAAAA
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ATTITIAAGTACTICTGGTTGATTATTTTA 3102 rrracagerreragacddcrraacrerrrr 7698 ATTITITATGAATTIAATTITATTICATATAA 3162 STATGATAATCTATTATCTATAGTAAAAA 7818 AIGTITGTIGAAATAAATTITGAAAGATTAT 3282 SATTATTGCAATAATGTATTATAATTTGTATT 3342 AAAAATAGTATCTTTTTAGT--TTTTAGT 3400 TICAAAAIGGGAAAGAIAITGTAITITAGA 3460 TIATCATCTTTTTATTTATTGCGACCAT 7100 ATGTTACAGATTATTTCCTAATATATCAGAA 2563 TTTATTAAGAATGTATCGAGCTTTTGAATAC 2623 AATAAAAAACATGGTCTAAGAATAAGATTTG 2683 ATTAGATTTAATAGAAATTAAATATATCAAT 7278 TTTGTGGCAATTCTTTTATCAAATGAAACG 2743 AAGTGACTTAGGTTTTGGTCATCCTAACTTT 7338 TGTCCAGATGAACTATTTATACAGACAATTA 2803 TCTAAATATGGAAATTTAAGATATATAAAGT 2863 TITACAGAIGATICIAI-TGAIGAATIGCIA 2922 ALTIATACTTATTATATATGTTACAAGAAT 7518 TAGAAAGTTAAAAATAGAAAATAAATCTAAA 2982 rgcrccdracarcacrgrrcrrgrragca 7578 ATAGTTGATTTTGTGAGAGTAATGTATGTTTA 3042 AAATGAAATTTTATTTTTTTATTATGGTCTA 3222 - TTTTGTTTATAATGTCTATAGTATTATTA 7873 Agagtrcactrggacggcaaaraaaaarragr 7993 TAACAGGCGTCAAAACAAGGTTGGTTGGCTT 3520 rrcrrgrraargargarcaacagargaragr 8113 TGTTGAATTTACAAAAGATGAGCAAAAATAT 2503 crtriararraacriraarrrrrrrrrcragc 7160

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4356 ATTTAAGTGGATCGAGAATTGGTAGTTTATCGCTAGCAATATTAA---TTATATGCTTGT 3696 CTAGAGAATCAAGTAACGAAGCTAGATTTATTATTATCAAGGAAGTATTGATAAAGTAT 3876 AAAATITITAAAAATAGATITATIGGICATAGICGAAAACITICIGIGATAGIITITCITA 8889 TATGAACTATCCTACGTTAAATACCACTACAATTATAGTTTCAATTCCGTTAATCTTTGC 3580 GGTTTTGTTGACAGCGACGATACAATTGACCCTAAAATGTATGAAACGTTACTAAATATA 8293 GTTAACTTATATAATAGACCTGAATACTATAATGTGCTTAATAAACAAGATTTCCTA 8413 TAGAAAACAATATTTTATTTGGATATGGAATATCCGGAATATTCAGTTACGGGAACTTGGC 3936 TCGGAAGTCATTCAGGCTATATATCATTTTTTTATAAATCAGGAATAGTTGGGTTGATTT 3996 TACTGATGTTTTTTTTTTTATGTTATAAAAAAGTTATGGAGTTAATGGGGAAACAG 4056 GATATCTGTACTGAGTGTTATTATTGCAAAGGATTTTA--ATGGATTTGAAGAAGTTG 8711 AGGATATGGAGACAAAAATGAATGATTTAATTTCAGTTATTGTACCAATTTATAATGTC 4236 ACTIATAAAAAATGCAACAATTITTTTTCTIGTGT-CTTGCTTTTATACCGATCT GAATGGAATGAACAAATTATGATGTCAATAAAATTACATATACTAGACAAGCTTATAAA AAAGAGTTATGTGAGGAGATAAGAAATCAGATGAAAGAATTAAGACATTTCACAAAACA TATGGAGATATATAGGTGGAAAATTTGCTTGGATAAAAAAGCTAATAGTAATATTTGTAA TACTACTTATTATATTACTGAATTGCTTTACCATGAAATTTTGGCTGTTTATAATT TACGAATTTCTGAGTACAATAAGATTTTTAGTTCAGTCTGCGAGGGGTTGTTATCTAGA GATTTAGCTTTAAAAATAAAATTCCGTGAAGAAAAAAAATATGAAGATACACAGTTTTAT rrrgarcrcaraaaargcraaraargrrrgrraraagccaaccrrrrraraarrac CACTATITITATITIACATCATTAGCCATATITITCATATATGAAACAATAGATCCGATTA TTATTATATTAGTACTATTCTTTCTTCAATAGGTATTTGGAATAATATAAAAA CTTTTCAAGATTATTGGTGCATATTCGTTAGTAGCTAATAAAATTGTATATAAAAG ATTATAGAAAAACCGAAGAATTAAGATAATAGCTTATTTTTTTCAAGAAAATTTATTG--GITATICICGIAAAIGAIGGAAGIACIGAIGAIICIGAGAAAAITIGCIIAAACIAIAIG AAGAACGATGGAAGAATTAAATTATACAAGAAAATTAATGGCGGTCTAGCAGATGCTCGA GAAGGAAAGTATGCTTTCGTGTTTATGCTAGATTGGATATTATTATCAATATGGT 4597 AATTTTCATGTCTTAACGAGAGAGAGACTGTAAAAGAATTTTTGTCAGGATCTAATATA AATGGAGGACAATCAAGCGCAAGGAATTTAAGGTATTTTATACTCTACAGGAGATTTGATT TACTACAGAAAAATAGTACAACAACTTCCTCATATAGTAGCTATCAATGGGACATAATC CAAGATTATCTTGATAAATGTATTAACAGTATTAATAACCAAACATATACTAATTTAGAG AATTTCGGACTAGAACATGCAACAGGTAAATATATTGCTTTTTGTCGATTCTGATGACTAT ATAGAAGTIGCAATGTICGAGAATGCATGATAATATAACTGAGTATAATGCCGATATA GAACTGTTATTAAAATGTATCAAATCATGGGAAAAATATTGTCCCAGATTACGAAATTATT 3757 8474 8712 4237 4297 8890 4357 4417 8234 3697 8294 3877 3937 8534 3997 8594 8654 4117 4177 8772 8950 6006

.0133 ACTTGAAACCGATCGTTAGTCGTTTAGAAGATTGTATTATATATTCTAGGGTGGAATTAT 10192 10085 ATAAAGTAGATATGGTTATCTGCAATTATTTGAGTGTTT------ATAATAATG 10132 9965 TATÓCGATGCTCGGAATTTTGGTGTAGTAAATGCTGAAGGGCGGTATATTTCTTTTATTG 10024 5676 5736 5196 5256 5316 5376 5077 TCAAGAAAGCATTTAGTTACGTTGTATTTGATGAAATTTTCGCCTAAACTATATGTAATG 5136 9844 TCAATITCAAGAATCCITITATAAAGAAAATATGAAAATCTACGAAG-ATACAGAATA 9364 ACACGTGTAGTAGTTGATACTAGAGAATATTATTATTATTATGTCATTCGTAACAGTTCG 4836 CTTATTAATCAGAAATTCTCTATAAATAATATTGATTTAGTCACAAGATTGGAGAATTAC 4896 CCCTTTAAGTTAAAAAGAGAGTTTAGTCATTATTTTGATGCAAAAGTTATTAAAGAGAAG 4956 GTTAAATGTTTAAACAAAATGTATTCAACAGATTGTTTGGATAATGAGTTCTTGCCAATA 5016 CTATAGTTTAAAAAAAAGGTGTGTGGCAATTACCACAGATTTACTAACAGAGCAAGGGCT 9424 TAAGTACATAAATAAAATTCAAGTAATAAACGGTATTTTAATTTTATCCTCCAAGTTATTT 9484 CCATTATGGACGAAATTGGGGAGGAGAAAAAAAAATAATTGATTTAGGTAGAATAAAGTT 9604 9605 AGGGGTTCATTTACTACTAGATAAGATATTTGGATATGGAACGTACAGAAATATTTAAA 9664 9665 GGCAGTAAAAAATAGTAAGGTATCAAAGGTAACCTGATTATTCATTTAAATAGTAATCT 9724 GAAAGTTATTTTGCTTGTGAGCT---ACCTGGAGAGGTTAATACAGGTTTGGGA AAGTGAATAATCCAAATATTGATTTTTGAAGCAATTAATACCGTGCAGGACATGGGAGAAA 10193 TTÄGTAATTTATÄTGGTAÄATATÄÄGGÄTCCTTTTACAÄCAGCCTGGGGAÄGTTTÄATAÄ 5677 AGAAAAGATACATAACAGATCTTTTCAAGAGAATCAATGGTTAGGAGAAGATTACTTT GAAAATAATGTTTGGTGCAAGCTTTATTCACGAGATATTATAAAAGATATAAAATTCCAA ATTAATAATAGAAGTATTGGTGAGGATTTGCTTTTTAATTTGGAGGTCTTGAACAATGTA TTAGAGICTTATCGAAAAGAAATACGTAGATATCCATTTAAAAGCGAAAAGATATTA TTATATAAGAAATTTCAAAAGCAGTAGAGGTAAAAATGGATAAAATTAGTGTTATTGTTC CAGTTTATAATGTAGATAATATTTAAGTAGTTGTATAGAAAGCATTATTAATCAAAATT ATAAAAATATAGAAATATTATTGATAGATGATGGCTCTGTAGATGATTCTGCTAAAATAT GCAAGGAATATGCAGAAAAAAAAAAAAAAGAGTAAAAATTTTTTCACTAATCATAGGGAG 9905 GTGATAATTATAGCCTGAAAGATAAACGAATCAGGGTATTTCATAAGAATAATGGAGGTT TATCAAATGCTAGAAATCATGGAATAAAGCGGAGTACAGCTGAATATATTATGTTG 5497 GTAGAAGTGATTTATCTGGTTGTTTGTACGCTACTTTTTCAGAAAATATAATTTTG 4657 1717 9425 5017 5137 5197 5257 5437 5557

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HQVDFLKELFLKYELDYILNISELENIIKEKNISTSKVISQNNDFCSSFKNELSKLFE
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Streptococcus agalactiae strain NCDC SS615 capsular polysaccharide
biosynthesis gene cluster, partial sequence.
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Direct Submission
Submitted (02-JAN-2001) CIDMLS, ICPMR, Westmead Hospital, Darcy
Submitted (02-JAN-2001) Australia
Rd., Sydney, NSW 2145, Australia
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                      5916 GACCTATCAATTGTTAAAGATACTATACGTTGGCAAGTATTTTATTATAGCTTACTAATG
                                                10313 CAACTTATAAATATTACTTATATTCAGATAAAATAGCCTTTGTACCAGAACCACTATATT
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Bacteria, Firmicutes, Lactobacillales, Streptococcaceae,
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TITLE
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1185	1244	Db 1304 CAGTTGATGATATGAAAGTATAATT	1204	1364	Db 1424 TAAAGTTAGALTTAGAATGATTAGATTAGATTAGATTAG	OY 1324 TAAAGACAGTGAAAGTTGTATTGTTGT 	1373	1544	Qy 1427 GITAAAACCGITITGGAAGGAAGAAGA 	Qy 1487 AAGAAGTCTTTTGAAGAATGAAAAA3		OY 1547 CATTAATTAGTGAAAAATAATTGTT DD 1724 CAAAAACTTGGTAAAAAAATACTATTGT	Qy 1607 TGTTATTATTCATCTGGTGCGGCCG		OY 1667 TGGAGCAAGAGGATTTATATTGAAGT 			Qy 1787 ATATCCTAAATCTATTAACTTGGGGA(1964	2024	Qy 1907 ATAACCGAAAATATTAFTCAAAC		DD 2144 TGGTCAAAAATITCTCAFTACAAAGAA	Qy 2027 ATTTGCCACGGAGGCCCCGCTACTTT		OY 2087 TIGTTTCCTAGACAAAAAGTAIGG
Best Local Similarity 59.2%; Pred. No. 2.6e-73; Matches 1390; Conservative 0; Mismatches 916; Indels 41; Gaps 7; 16 TGGCATTATTTGATAGCAGTTGCAATTTCTGCAATCTTAACAAGTCATATACCAA 75			233 CICCCCAATITTAAAAGCAATAAAGATTTATTGTTCTATTGATACATTATATTGTCT 292 133 TTTTTATATCTCGTATGCCAGTTGAATTTGAGTATAGAGGTAATCTGATAGAGTTTGAAA 192		193 AAACATITAACTATAGTATAATATTTTGCAATTTTTCTTACGGCAGTATCATTTTTGTTGG 252 153 HGCGTATTTTTGTTGG 252					533 CACGAGATACCAAAGFTGTTTTGATAACGAATAAGGATTCTTTATCAAAAATGACCTTTA 592 433 TATTTGAATCACATAAACAAATTCAAAAAAATCTTGTTGCTTGC	GGAATAAATACGACCATAATATATATATGCTGTCTGCATCTTGGACTCCTCTGAAAAGG		650 ATTGTTATGATTTGAAACATAACTCGTTAAGGATAATAAACAAAGGATGCTCTTACTTCAG 709	AGTTAACCTGCTTAACTGTTGATCAAGCGTTTATTAACATACCCATTGAATTTTAGTTA	613 TAAAGCAATTCGTTTCAGATTTTGAGTTGTTAGGTATTGATGTAAGCGTTG 663	770 AATACCAAATACAAGATATTATTAATGACATTGAAGCAATGGGAGTGATTGTCAATGTTA 829	664 ATATTAATTCATTCGGTTTTACTGCGTTGAAAAAACAAAAAATCCAACTGCTAGGTGACC 723 	TTTTTCCACAAATTTTTATAAGCCTAGTCATATCATGAAACGAC	890 ATAGTGTTATTACATATTCTATGAAATTCTATAAATATAGTCACCTTATAGCAAAACGAT 949	784 TTTTGGATATACTCGGAGCGGTAGTCGGGTTAATTTGTGGGTATAGTTTCTATTTGT 843			ATTTACATTCTACAAGTTTCGATCGATGTATGTTGATGCTGAGGAGC	10/0 GIAATGGTAGGATTTTTAGATTCTATAAATTCAGATGAATGCGAGTAGATGCAGAAGAA 1129 064 GCAAAAAAAGATTTGCAGAAAAAACAAAAAAAAAAAAAA	TTAAGAAAGATTTATTAGTTCACAATCAAATGACAGGGCTAATGTTAAGTAAGA	1024 AAACGATCCTAGAATTACTCCAATTGGACATTTCATACGCAAAAACAAGTTTAGACGAGT 1083
Bes Mat	qq	ठें व	8 8	셤	ð f	8 8	g 8	3 8	8 1	8 8	2 점	ò	음 &	5 A	ò	qa	<i>장</i> 옵	ò	qq	ð á	3 8	7 음	à i	g è	岩	∂ .

TAATTGGACTATCTGGTCAGATATTAAAATTTAT 1323 GGTTCTTCAGGGGGACATTTGACTCACTTGTATTT 1426 BAACGTTTTGGGTAACATTTGATAAAGAGGATGC 1486 ATTTTATTGTTCAGTGGGAAGAAATGAAGAAGGT 1786 AGTATTTTTAATGATTTTTGTAACAGTAGGAACT 1846 TAAAAGAGATTGATTATTGAAAAAAAAAGAGT 1906 1966 2143 2026 2203 ITATGAATTCATTATCCAAAGGAAAAAAAAATTA 2086 GTGAACATGTAAATGATCATCAAGTAGAGTTTGTA 2146 FGGCGATATGAGTCTAGTTGGTACACGTCCACCTA 1143 regregragiantarea de la 1263 ATGTATCCATGTTACTTTCCAACAAATCGCAATCT 1546 GTATATCATTGCTTCTTTCCAACAAACCGTAATGT 1723 CTAGCTTTTAAGGTCCTTAGAAAAGAAAGACCAGA 1783 STIGCIGICCCCTTCTTIACAICGGAAAACTAIT 1666 STATITICATICGAGITAATAAATCTACATTAACTGG 1726 CCTGGTCAAAAGACGATTGAGTTTTAAACCAG 1203 TCAACGCAGAAGCGACGCCTTAGTTTTAAGCCAG 1363 TTAGCTTTCAAAATTTTACGTGATGAGAAACCAGA 1606 SGAAAATTTATTCG-AAAAACAAGCATAGATGAGT 1243 atàticaactettacatgaaagaagctgagattgtt |||||||||| |TATGAATGCAGTTTCTAAAGGGAAAAAAACTATT CAGGATATTCTGACTATATTCCAGAATATTGCAAG AAATGGAACAATATATTAACAAATCAGAAGTAGTT

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                                                                                                                                                                              product="CpsF"
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                                                               2324 AAAGAGTTATTCTTGAAATATGAATTAGATTATATTTTGAATATCAGTGAATTAGAGAAT 2383
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                                                                                                                                                                                                                                                BCT 07-JAN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                   4513 bp DNA linear BCT 07-JAN-20
Streptococcus agalactiae strain SG99/077 capsular polysaccharide
biosynthesis gene cluster, partial sequence.
AF363060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cong. F. and Gilbert, G.L.
Kong, F. and Gilbert, G.L.
Direct Submission
Submitted (22-MAR-2001) CIDMLS, ICPMR, Westmead Hospital, Darcy
Road, Sydney, NSW 2145, Australia
Location/Qualifiers
                     AAAATTATTGAAGTTTCTAAGCAAAC---TAACTTTACATCAAATAATATTTTTTTGT
                                                                                                                                                      2384 ATTATTAAGGAAAAAATATATCTACTAAAGTAATATCACAAAACAATGATTTTTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kong, F., Gowan, S., Martin, D., James, G. and Gilbert, G.L. Serotype identification of group B streptococci by PCR and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptococcus agalactiae
Bacteria, Firmicutes, Lactobacillales, Streptococcaceae,

    4513
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product="CpsE"
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gene="cpsE"
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Best Local Similarity 59.2
Matches 1390; Conservative
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SS700 capsular polysaccharide
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Kong,F. and Gilbert,G.L.
Direct Submission
Submitted (02-JAN-2001) CIDMLS, ICPMR, Westmead Hospital, Darcy
Rd., Sydney, NSW 2145, Australia
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                         Kong.F., Gowan,S., Martin,D., James,G. and Gilbert,G.L. Serotype identification of group B streptococci by PCR and
                                                                                                                                                                                                                                                                                      Streptococcus agalactiae
Bacteria, Firmicutes, Lactobacillales; Streptococcaceae;
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Streptococcus agalactiae strain NCDC SS700 cs
biosynthesis gene cluster, partial sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                       J. Clin. Microbiol. 40 (1), 216-226 (2002)
21635022
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2324 AGATGCA
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SOURCE
ORGANISM
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VERSION
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TITLE
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AF332914
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Qy 1427 GTTAAAACCGTTTTGGAAGGAAGAACGTTTTTGGGTAACATTTGATAAAGAGGATGC 1486	OY 1487 AAGAAGTCTTTTGAAGAATGAAAAAAGTGTTCCATGTTACCTTTCCAACAAATGCAATCT 1546	Qy 1547 CATTAATTTAGTGAAAAATACTTTCTTAGGTTTCAAAATTTTACGTGATGAGAAACCAGA 1606 	Qy 1607 IGTARITALITCAECTGGGGCGGTGGTGCTGCCCTTCTTTACAECGGAAAACTAIT 1666	OY 1667 TGGAGCAAAGACGATTTATATTGAAGTATTTGATCGAGTTAATAAATCTACATTAAACTGG 1726	QY 1727 AAAACTAGTTTATCCGGTAACAGATATTTTTTTTGTTCAGTGGGAAGAATGAAGAGGT 1786	Qy 1787 ATATCCTAAATCTATTAACTTGGGGAGTATTTTTTAATGATTTTTGTAACAGTAGGAACT 1846	Oy 1847 CATGAACAACAGTTTAATGATTGATAAAAGAGATTGATTTATTGAAAAAA	Qy 1907 ATAACCGAGGAAATATTATTGAAACAGGATATTCTGACTATTCCAGAATATTGCAAG 1966	QY 1967 TATAAAAATTTCTCAGTTACAAAGAAATGGAACAATTAATT	OY 2027 ATTTGCCACGGAGGCCCCGCTACTTTTATGAATTCATTATCCAAGGAAAAAACAATTA 2086 1	Qy 2087 TTGTTTCCTAGACAAAAAGTATGGTGAACATGTAAATGATCATCAAGTAGAGTTTGTA 2146 Db 2273 GTGGTTCCTAGACAAGAACAGTTTGGAGAGCATGTGAATAATCATCAGGTGGATTTTTG 2332	Qy 2147 AGAAGATTTTACAAGATAATATTTTATTTATTAGAAATATAGATGATTTGTTTGAA 2206 Qy 2117	Qy 2207 aaaattattgaagtttctaagcaaactaactttacatcaaataataattttttgt 2263 	Qy 2264 GADAGATTAAAACAAATAGTTGAAAAATTTAATGAGGATCAAGAAAAATGAATAAAAA 2323 Db 2453 TCCTCTTTCAAAAATGAACTTTCTAAACTATTTGAATAATTTTGTTGGAGAAAAA 2512	Qy 2324 AGATGCA 2330 Db 2513 AATTGAA 2519	RESULT 16 AF332893 AF332893 LOCUS LOCUS DEFINITION Streptococcus agalactiae strain 090 capsular polysaccharide biosynthesis gene cluster, partial sequence. ACCESSION AF332893.1 GI:18033311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               362 IGGIÁITGAAATÁCAÓCTÍTTACTATATTTTCATATCAÁGTTCATTÁTTTTTTTTTA 421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            133 TITITATATCTCGTATGCCAGTTGAATTTGAGTATAGAGGTAATCTGATAGAGTTTGAAA
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Matches 1390; Conservative
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                                                                                                                                                                                                                                                    Z (bases 1 to 4888)
Kong, F. and Gilbert, G.L.
Direct Submission
Submitted (02-JAN-2001) CIDMLS, ICPMR, Westmead Hospital, Darcy
                                                                                                                      Kong, F., Gowan, S., Martin, D., James, G. and Gilbert, G.L. Serotype identification of group B streptococci by PCR and
             Streptococcus agalactiae
Streptococcus agalactiae
Bacteria, Firmicutes; Lactobacillales; Streptococcaceae;
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1 (bases 1 to 4888)
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Matches 1390; Conservative
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Kong,F. and Gilbert,G.L.
Direct Submission
Submitted (22-MAR-2001) CIDMLS, ICPMR, Westmead Hospital, Darcy
Road, Sydney, NSW 2145, Australia
Location/Qualifiers
                                                                                    Streptococcus.
I bases I to 4888)
Kong,F., Gowan,S., Martin,D., James,G. and Gilbert,G.L.
Serotype identification of group B streptococci by PCR and
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AF363057 4888 bp DNA linear BCT 07-JAN-2002 Streptococcus agalactiae strain GB00/017 capsular polysaccharide biosynthesis gene cluster, partial sequence. AF363057.1 GI:18029155

RESULT 18 AF363057 LOCUS DEFINITION

ACCESSION VERSION

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YMKLRNYSIMTĪGVVLLFTFILÞIGSGSRAGIVAILAOMFILLINTVVVKKKTIKFLL
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Best Local Similarity 59.2%;
Matches 1389; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                     ICPMR, Westmead Hospital, Darcy
                                                                                            Streptococcus.
I bases I to 4888)
Kong, F., Gowan, S., Martin, D., James, G. and Gilbert, G.L.
Serotype identification of group B streptococci by PCR and
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Streptococcus agalactiae
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J. Clin. Microbiol. 40 (1), 216-226 (2002)
21635022
                                                                                                                                                                                                                                                                                        2 (bases 1 to 4888)

Kong, F. and Gilbert, G.L.

Direct Submission

Submitted (2-MAR-2001) CIDMLS, IC

Road, Sydney, NSW 2145, Australia

Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       <u>raeceargaricaaacagricigeririaririririciecaagririgacarraacarraatra</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      242 cicccaairiraaaagcaaraaagarrrarrgrirgrircrarrgaracarrargrer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                302 TTTATCTTTCTGATTTTTACAGAGACTTTTGGAGTCGTGGCTATCTTGAAGAGTTTTAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           193 AAACATTTAACTATAGTATAATATTTGCAATTTTTTTTTGCTGGGAGTATCATTTTTGTTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      253 AGAATAATTTCGCACTTTCAAGACGTGGTGCCGTGTATTTCACATTAATAAACTTCGTTT
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gene="cpsH"
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                                                                                                                                                                                                                                                                                                                              ICPMR, Westmead Hospital, Darcy
                                                                                     Streptococcus.
I bases 1 to 4888)
Kong.F., Gowan,S., Martin,D., James,G. and Gilbert,G.L.
Serotype identification of group B streptococci by PCR and
                  Streptococcus agalactiae
Streptococcus agalactiae
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;

    .4888
/organism="Streptococcus agalactiae"
/mol.type="genomic DNA"
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J. Clin. Microbiol. 40 (1), 216-226 (2002)
21635022
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Kong, F. and Gilbert, G.L.

Direct Submission

Submitted (22-MRR-2001) CIDMLS, IC

Road, Sydney, NSW 2145, Australia

Location/Qualifiers
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db_xref="GI:18029172"
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Miyake, K., Watanabe, M. and Iijima, S.

Miyake, K., Watanabe, M. and Iijima, S.

Miyake, K., Watanabe, M. and Iijima, S.

Miyake, K., Watanabe, M. and Iijima, S.

Beta-1, 3-galactosyltransferase and DNA encoding the enzyme

Patent: JP 2002199885-A 2 16-JUL-2002;

KYOWA HAKKO KOGYO CO LTD

OS Streptococcus agalactiae Type Ib

PN JP 2002199885-A/2

PD 16-JUL-2002

PP 05-JNN-2001 JP 2001000392

PP 05-JNN-2001 JP 2001000392

PP KATSUHIDE MIYAKE, MASAKI WATANABE, SHINJI IIJIMA PC

CIZNI5/09,CIZNI/21,CIZNY/10,CIZPI9/28/CIZNI5/09,CIZNI1:46)

CIZNI5/09. (CIZNI5/19),(CIZPI9/28,CIZRI:19),CIZNI5/00, PC

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Pred. No. 3.5e-73;
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[617] . (1789)
(1816) . (2262)
(2265) . (2744)
(2863) . (3979)
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(5009) . (5947)
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(E-mail:miyake@proc.nubio.nagoya-u.ac.jp, Tel:81-52-789-4278,
Fax:81-52-789-3221)
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/db_xref="taxon:1311"
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2842. .3981
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                                                                                                                                                                               1787 ATATCCTAAATCTATTAACTTGGGGAGTATTTTTAATGATTTTTGTAACAGTAGGAACT 1846
                                                                                                                                                                                                         2229 TTATCCTAAGGCAATTAATTTAGGAGGAATTTTTTAATGATTTTTGTCACAGGGGGGACA 2288
                                                                                                                                                                                                                                                                TATAAAAAATTTCTCAGTTACAAAGAAATGGAACAATATAATAACAAATCAGAAGTAGTT 2026
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Sch. of Engineering, Dept. of Biotechnology; Chikusa-ku, Furo-cho,
Nagoya, Aichi 464-8603, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptococcus agalactiae cpslbb, cpslbF, cpslbG, cpslbH, cpslbI, cpslbK, cpslbK, cpslbL, neuC genes, complete cds.
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CpsJ of Streptococcus agalactiae type Ib shows
Desl, 3-galactosyltransferase activity
Unpublished
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Miyake, K., Watanabe, M. and Iijima, S.
Direct Submission
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Streptococcus agalactiae
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                                                                                                                                                                                                                                                                                                         function="beta-1,3-N-acetylglucosaminyltransferase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     function≃"putative repeat unit transporter"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LYICLYLYFKSPLVRRLLINDINILVLKLFGGEKQSD"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   556
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   193 AAACATTTAACTATAGTATAATATTTGCAATTTTTCTTACGCCAGTATCATTTTTGTTGG 252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     796
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     492
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTCCCAACTTTAAAAGCAATAAAGATTTATTGTTTGTTCTATTGATACATTATATTGTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTTATCTTTCTGATTTTTACAGAGACTTTTGGAGTCGTGGCTATCTTGAAGAGTTTAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGAATAATTTCGCACTTTCAAGACGTGGTGTGTATTTCACATTAATAAACTTCGTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                <u> Aaaacreritracaacacacacritrecrrrritractitratrecrateaarrecatitr</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TATTATATTCTATTCAATTTTTAAAATATTATCGAAAATATTCTTACGCTAAGTTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 9987;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            function="sialic acid synthetase"
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59.2%; Pred. No. 3.1e-73;
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JOURNAL J. Clin. Microbiol. 40 (1), 216-226 (2002) MEDLINE 2163502 PUBMED 11773119 PEREPENSE 1 10 4768)	1547 CATTAATTTAGTGAAAATACTTTCTTAGCTTTCAAAATTTTACGTGATGAGAAACCAGA 1606 	∂ 6
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RESULT 22 AP332896 LOCUS AP332896 AP332896 AP332896 AP332896 AP332896	1324 TAAAGACAGTGAAAGTTGTTGACAGAGGGAAGTAAGTAAAGTA 1372 	ζό O
Db 2768 AATTGAA 2774	1264 TTCGGTTGGACTTAGCATACATTGATAATTGGACTATCTGGTCAGATATTAAAATTTTAT 1323 	QV Db
2708	1204 GGATTACAGGTCTCTGGCAGGTTAGTGGTCGTAGTAATATCACAGACTTCGACGACGTAG 1263 	çy G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   233 CTCCCAATTTTAAAAGCAATAAAGATTTATTGTTTGTTCTATTGATACATTATATTGTTT 292
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    493 AAATAGATAAAATTAATTTATCATTACCGCTCTATTATTCTGTGGAAGAAGCTATAGAGT 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTGTTATGATTTGAAACATAACTCGTTAAGGATAATAAACAAAGATGCTCTTACTTCAG 709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    433 TATTIGAATCACATAAACAAATTCAAAAAATCTTGTTGCATTGGTAGTTTTAGGTACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      76 ATGCTGATTTAAATCG---TTCTGGAATTTTTATCATAATGATGGTTCATTATTTTGCAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            293 TTTATCTTTCTGATTTTTACAGAGACTTTTGGAGTCGTGGCTATCTTGAAGAGTTTTAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGAATAATTTCGCACTTTCAAGACGTGGTGCCGTGTATTTCACATTAATAAACTTCGTTT
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); Mismatches 902;
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Best Local Similarity 59.2
Matches 1366, Conservative
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                                        Dmitted (02-JAN-2001) CIDMLS, I
., Sydney, NSW 2145, Australia
Location/Qualifiers
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Kong, F. and Gilbert, G.L. Direct Submission Submitted (02-JAN-2001)
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Gaps

75

132

192 352 412 312 472 492

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AF363055 4768 bp DNA linear BCT 07-JAN-2002 Streptococcus agalactiae strain SG99/143 capsular polysaccharide biosynthesis gene cluster, partial sequence.
                                                                                                                                                                                                                                           1787 ATATCCTAAATCTATTAACTTGGGGAGTATTTTTAATGATTTTTTGTAACAGTAGGAACT 1846
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Kong, F. and Gilbert, G.L.

Direct Submission
Submitted (22-MAR-2001) CIDMLS, ICPMR, Westmead Hospital,
Road, Sydney, NSW 2145, Australia
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptococcus agalactiae
Streptococcus agalactiae
Bacteria, Firmicutes; Lactobacillales; Streptococcaceae;
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1 (hases 1 to 4768)
Kong. F., Gowan, S., Mattin, D., James, G. and Gilbert, G.L. Serotype identification of group B streptococci by PCR
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J. Clin. Microbiol. 40 (1), 216-226 (2002)
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KEYWORDS
SOURCE
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LDYILFKTNLKLTKGNFICHTFTAFFSYNWSIIEKIIMYROSTITRMIVYQ
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'translation="AKEQMEQSGSKFLGIILNKVNESVATYGDYGNYGKRDRKRK"
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AF363056 4768 bp DNA linear BCT 07-JAN-2002 Streptococcus agalactiae strain GB00/031 capsular polysaccharide biosynthesis gene cluster, partial sequence.
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Streptococcus agalactiae
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
Streptococcus.
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Kong,F., Gowan,S., Martin,D., James,G. and Gilbert,G.L.
Serotype identification of group B streptococci by PCR a
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                                                                                                                                                                                                                                       TITIGGATATACTCGGAGCGGTAGTCGGGTTAATTATTTGTGGTATAGTTTCTATTTTGT 843
                                                                ATATTAATTCATTCGGTTTTACTGCGTTGAAAAACAAAAAATCCAACTGCTAGGTGACC 723
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                                                                                                      ATGTAGAGGCACTTAGCTTTGATAATATAGGAGAAAAGCGAATCCAAACTTTTGAAGGAT
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NSGEI CDNLSQEDNR I LVFHKKNGGVSSARNLGLDKSTGEF I TFVDSDDFVAPNMI E I
MLKNL I TENAD I AEVDFD I SNERDYRKKKRRNFYKVFKNNNSLKEFLSGNRVEN I VCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     413 AAAACTCTTTTACAACGACACCACTTTTCCTTTTTTACTTTTATTGCTATGAATTCGATTT 472
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCTATCAAAAAAAGACGATTCTAATTACAACGGCTGAACGATGGGAAAATATGCAAGTTT 432
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 726.8; DB 1; Length 4768;
Pred. No. 5.1e-73;
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                                                                                                                                                                                                                                                                                                                                                          /product="CpsJ"
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DLKHNSLR I INKDALTSELTCLTVDQAFINIPIELFGKYQIQDIINDIBAMGVIVNVN
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178. .1527
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/gene="cpsH"
                                                                                      gene="cpsD"
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AF163833 17276 bp DNA linear BCT 03-AUG-2000 Streptococcus agalactiae capsular polysaccharide synthesis locus, complete sequence.
AF165833 L09116
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2 (Dases 15471 to 16670)
Haft, R.F., Wessels, M.R., Mebane, M.F., Conaty, N. and Rubens, C.E.
Characterization of cpsF and its product CMP-N-acetylneuraminic
acid synthetese, a group B streptococcal enzyme that can function
in K1 capsular polysecotaride biosynthesis in Escherichia coli
Mol. Microbiol. 19 (3), 555-563 (1996)
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Chaffin, D.O., Beres, S.B., Yim, H.H. and Rubens, C.E.
The serotype of type Ia and III group B streptococci is by the polymerase gene within the polycistronic capsule J. Bacteriol. 182 (16), 4466-4477 (2000)
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Rubens, C.E., Heggen, L.M., Haft, R.F. and W
Identification of cpsD, a gene essential
expression in group B streptococci
Mol. Microbiol. 8 (5), 843-855 (1993)
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QINSPHILKOKLPWINKHRRPKKRARYFLEENLVHFVASDMHNLDVRPPFLAEAYKIIC
RDFGKERANQLFIENAQSILKNHYI"
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db_xref="GI:1323730"
'translation="MTRLBIVDSKLRQAKKTBEYFNAIRTNIQFSGKENKILAIASVR
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DAAI I ANACDGFI LVTQAGRI KRNY VEKAKEQMEQSGSKFLGI I LNKVNESVATYGDY
GNYGKRDRKRK"
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LINSFLKYYRAFRSPATRYLLTHYNDSLSKATFRNKYDHYTAVCILDSSENDCY
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FKPGITGLMQISGRNNITDFDBIYKLDVQYINEWSIWSDIKIILLTLKVVLLGTGAK
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|db_xref="GI:5823212"
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/note="glucosyl transferase; previously described as CpsD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="putative polysaccharide chain length regulator"
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note="CPS chain length regulator/exporter"
                                                                                             function="tyrosine phosphatase"
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3316. .3321
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NRKNYPHKEGYENIYYSGIDFFGSISTVSRESDYNIMAYVSLIELSTPDFKSQIKTIYTYKIKKKI
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GELPSYAMPGAQLYMMSIDQSSLSNAKSKIKNTMEE"
2570. 3317
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                                                                                                                                                                                                  Direct Submission
Submitted (16.MAX-1996) Division of Infectious Disease, Immunology
and Rheumatology, Children's Hospital and Regional Medical Center,
4800 Sand Point Way N.E., Seattle, WA 98105, USA
6 (bases 1 to 17276)
Chaffin,D.O., Yim,H.H., Beres,S.B., Sweet,E.S., Nittayajarn,A. and
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TNNLNKTASYSEI EMSVVVPKOSKITNI EAVSKLAAPVKNDTSNITDLIEHIKSEKGI
                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (29-JUN-1999) Division of Infectious Disease, Immunology and Rheumarology, Children's Hospital and Regional Medical Center, 4800 Sand Point Way N.E., Seattle, WA 98105, USA On Sep 5, 1999 this sequence version replaced gi:1323729.

Location/Qualifiers
                                                                                        Submitted (27-JAN-1993) Division of Infectious Disease, Immunology and Rheumatology, Children's Hospital and Regional Medical Center, 4800 Sand Point Way N.E., Seattle, WA 98105, USA 5 (bases 4495 to 6194)
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/ransi table=11
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/organism="Streptococcus agalactiae"
/mol_type="genomic DNA"
/strain="COH1"
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db_xref="GI:5823211"
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complement(7..930)
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                                                                      Direct Submission
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/function="beta-1,4-galactosyltransferase"
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function="beta-1,4-galactosyltransferase
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0; Mismatches 902;
                                                                                                                               /protein_id="AAD53067.1"
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	Description	Aaz60930 Nucleotid	Aaz60929 Nucleotid	Aba01441 Streptoco	Ads13200 S. thermo	Continuation (12 o	Abk90550 Beta1,3-g	Aca64723 Streptoco	Adf43363 Sterptoco	Ado40235 S. agalac	Adm79774 Group B S	Aah43197 Portion o	Aas55950 Streptoco	Adr93668 Novel S.	Aba01446 Streptoco	Aaz30355 Nucleotid	Aaz45258 DNA encod	Aba01447 Streptoco	Aba01445 Streptoco	Aba01443 Streptoco	Aba01444 Streptoco
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	Score	6992	1195.8	955.6	889	798.8	727.8	726.8	726.8	721.4	649.2	428.4	423.2	415.8	383.2	376.2	376.2	376	373	371.6	371.4
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ABA01436	ABA01442	ABA01448	ABA01435	ABA01433	ABA01440	ABN70387	ABN67429	ABA01439	ABZ10246	ABZ10246	ABA01437	ADC50017	ABN67430	ABA01438	ABZ10100	ABZ10100	ABL55643	ABA01434	AAS45313	ABK28152	ABL55643	ABK28258	ABL34241	
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371.4	366	364.8	347.2	346	332	320.2	320.2	314.8	301.4	298.8	291.6	283.8	255	230.2	222.2	219.8	206.6	198.4	187.8	187.8	185.8	183.6	179	
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                                                                                                                                                                                                                           New nucleic acid containing the capsular gene cluster of Streptococcus suis, used for serotype-specific detection and to generate antigens or mutants for vaccination.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAAGTCATATACCAAATGCTGATTTAAATCGTTCTGGAATTTTTATCATAATGATGGTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TAGAGITIGAAAAAACATITAACTATAGTATAATATITGCAATTITTCTTACGGCAGTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TAAACTICGTTTTGGTATACCTATTTAACGTAATTATTAAGCAGTTTAAGGATAGCTTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATCGCCAAACGAAATTGGCATTATTTGATATGATAGCAGTTGCAATTTCTGCAATCTTAA
             termination codon
                                                                                                                                                                                     WPI; 2000-195104/17.
P-PSDB; AAY68970, AAY68971, AAY68972, AAY68973, AAY68974, AAY68975,
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                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 6992 BP; 2513 A; 788 C; 1214 G; 2477 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 3; Length 6992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
             얺
                                                                                                                                                                                                                                                                                                                                                                                                           humans or animals, e.g. against S. suis in pigs
            encodes AAY68976;
                                                                                                                                           (DIEN-) STICHTING DIENST LANDBOUWKUNDIG ONDERZOE
                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 6992; 100.0%; Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
g
"Cps1K;
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                                                                                                          98EP-00202465
                                                                                      99WO-NL000460
                                                                                                                     98EP-00202467
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  /*tag=
/note=
given"
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                                            WO200005378-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Simil
Matches 6992; C
                                                                                    19-JUL-1999;
                                                                                                          22-JUL-1998;
                                                                                                                    22-JUL-1998;
                                                                03-FEB-2000
                                                                                                                                                                                                          AAY68976.
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                                          480
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                           ATATGCAAGTTTTATTTGAATCACATAAACAAATTCAAAAAAATCTTGTTGCTTGGTAG
                                                                                                                       TTTTAGGTACAGAAATAGATAAAATTAATTTATCATTACCGCTCTATTATTCTGTGGAAG
                                                                                                                                                                                                                  AAGCTATAGAGTTTTCAACAAGGGAAGTGGTCGACCACGTCTTTATAAATCTACCAAGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GACTTTTGGATATACTCGGGGGGGGTGGGTTAATTTGTGGGTTTCTATTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAAAAACGATCCTAGAATTACTCCAATTGGACATTTCATACGCAAAAACAAGTTTAGACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAAAAAACGATCCTAGAATTACTCCAATTGGACATTTCATACGCAAAAACAAGTTTAGACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGTTACCACAGTTTTATAATGTTTTAATTGGCGATATGAGTCTAGTTGGTACACGTCCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGAAGGAAGAACGTTTTTCGTAACATTTGATAAAGAGGATGCAAGAAGTCTTTTGA
ATATGCAAGTTTTATTTGAATCACATAAACAAATTCAAAAAAATCTTGTTGCATTGGTAG
                                                                                         TITIAGGIACAGAAATAGATAAAATTAATTTATCATTACCGCTCTATTATTCTGTGGAAG
                                                                                                                                                                                       AAGCTATAGAGTTTTCAACAAGGGAAGTGGTCGACCACGTCTTTATAAATCTACCAAGTG
                                                                                                                                                                                                                                                                                     AGTTTTTAGACGTAAAGCAATTCGTTTCAGATTTTTGAGTTGTTAGGTATTGATGTAAGCG
                                                                                                                                                                                                                                                                                                                                    AGTTTTTAGACGTAAAGCAATTCGTTTCAGATTTTTGAGTTGTTAGGTATTGATGTAAGCG
                                                                                                                                                                                                                                                                                                                                                                                 TTGATATTAATTCATTCGGTTTTACTGCGTTGAAAAACAAAAAATCCAACTGCTAGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                ACCATAGCATTGTAACTTTTTCCACAAATTTTTATAAGCCTAGTCATATCATGATGAAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TAGTICGGTIGGACTIAGCATACATIGATAATIGGACTATCTGGTCAGATATTAAAATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1261 TAGTTCGGTTGGACTTAGCATACATTGATAATTGGACTATCTGGTCAGATATTAAAATTT
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2581 ACTGTTTAGAATTTTATTAAGAATGTATCGAGCTTTTGAATACTATTTACAAAGATTGTT 2640 2641 GTTTATTGATAGAATAAAAACATGGTCTAAGAATAAGATTTGGTTCTAATTGGTTCTCG 2700 2641 GTTTATTGATAGAATAAAAACATGGTCTAAGAATAAGATTTGGTTCTAATTGGGTTTCG 2700 2701 CTTCCACATGATTTTGTGGCAATTCTTTTATCAAAAGAATTTGGTTCTAATTGGGTTTCG 2700 2701 CTTCCACATGATTTTGTGGCAATTCTTTTATCAAATGAAAACGAAACAGATTATTTTT 2760 2761 AAGTAATCTAAATGTCCAGATGAACTATTTATACAGACAATTATATAGAAAAATTATTT 2760 2761 AAGTAATCTAAATGTCCAGATGAACTATTTATACAGACAATTATATAGAAAATTTTT 2820 2761 AAGTAATCTAAATGTCCAGATGAACTATTTATACAGACAATTATAGAAAATTT 2820	2821 TCAAATAGATTATCTAAATATGGAAATTTAAGATATATAAAGTGGAAAAATCAACATCT 2880 2821 TCAAATAGATTATCTAAATATGGAAATTTAAGATATAAAAGTGGAAAAAATCAACATCT 2880 2881 TCTCCTATTGTCTTTACAGATGATTCTATTGATGAATTGCTAAATGCAAAAATTTAGGT 2940 2881 TCTCCTATTGTCTTTACAGATGATTCTATTGATGAATTGCTAAATGCAAGAAATTTAGGT 2940 2941 TTTTTATTTGCTTAGAAAGTTAAAAATAAAAATAAAAAATTTAAAGAAATTTACT 3000 2941 TTTTTATTTGCTAGAAAGTTAAAAAATAAAAATAAAAATTTAAAGAAATTATACT 3000	3001 AAAAATAAAATAGTTGATTTGTGAGAGTAATGTTTAAATTATT	3181 TAATATTAAAAAATGAAATTTTATTGITTTTATTGTCTATATTATGTTTTGTG 3240 3181 TAATATTAAAAATGAAATTTTATTGTTTTATGGCCTATATTATGTTTGG 3240 3241 TAGTCACAAGTATGTTGTTGAATAATTTTGAAAGATTATTTGCAGATTTTACTGCTC 3300 3241 TAGTCACAAGTATGTTGTTGAATAATTTTGAAAGATTATTTGCAGATTTTACTGCTC 3300 3241 TAGTCACAAGTATGTTGTTGAATAATTTTGAAAGATTATTGCAGATTTTACTGCTC 3300 3301 CCATAATTTGGATTATTGCAATAATGTATTATAATATTGTATTATAAAATATTGATT 3360 3301 CCATAATTTGGATTATTGCAATAATGTATTATAATATTGTATTATAAAATATTGATT 3360		3541 ATACCACTACAATTATAGTTTCAATTCCGTTAATCTTTGCACTTATAAAAAATAAAATGC 3 [1
	CCGTAACAGATATTTTTATTGTTCAGTGGGAAGAATGAAGGTATATCCTAAATCTA CCGTAACAGATATTTTTTTTTT	ATTIATTCAACAGGATATTCTGACTATATTCCAGAATATTGCAAGTATAAAAATTTCT ATTIATTCAAACAGGATATTCTGACTATATTCCAGAATATTGCAAGTATAAAAAATTTCT ATTIATTCAAACAGGATATTCTGACTATATTCCAGAATATTGCAAGTATAAAAAATTTCT CAGTTACAAAGAAATGGAACAATATTAAACAATCAGAAGTAGTTATTTGCCACGGAGG	CCCCGCTACTITTATGAATTCATTATCCAAAGGAAAAAACAATTATTGTTTCCTAGACA AAAAAAGTATGGTGAACATGTAAATGATCCAAAGGAAAAAAGTTGTATGTTTCCTAGACA AAAAAAGTATGGTGAACATGTAAATGATCATCAAGTAGAGTTTGTAAGAAGAATTTTACA AGATAATAATAATTTTATTATAGAAAATATAGATGATTTGTTTGAAAAAA	2221 TTCTAAGCAAACTATACATCAAATAATTTTTTTTTTTTT	TATTC 2460 ATATA 2520 ATATA 2520 ATGT 2580 ATGT 2580 TTGTT 2640

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*tag= c
transl_except= (pos: 2916. .2918, aa: Xaa)
note= "ORF 2X; Xaa is an unspecified amino acid; encodes
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an unspecified amino acid; encodes
                                                                                                                                                                                                                                                                                                                  Capsular gene cluster; serotype 2; polysaccharide biosynthesis; capsular component; antigen; regulation; chain length determination; complement-mediated opsonophagocytosis; serotype-specific detection; antigen; vaccine; Streptococcal disease; ORF 22; ORF 27; ORF 22; Cps2A; Cps2B; Cps2C; Cps2D; Cps2B; Cps2C; Cps2B; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; Cps2C; C
                                                                                                                                                                                                                                                                            S. suis serotype
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amino acid;
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                                                                                                                                                                                                                                                                         Nucleotide sequence of a capsular gene cluster of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= a
/note= "ORF 2Z; encodes AAY68950"
complement(822. 2079)
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note= "ORF 2Y; encodes AAY68951"
:202. .2936
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'note= "Cps2F; encodes AAY68958"
0262. .10419
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note= "Cps2C; encodes AAY68955"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note= "Cps2E; encodes AAY68957"
089. .9258
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.18904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            *tag= d
'note= "Cps2A; encodes AAY68953"
504. .5193
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note= "Cps2B; encodes AAY68954"
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          6961 ATCATTGGTTGAGCAAACAGCAAAAGAAGCTT 6992
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/transl except= (pos: 1.
/note= "Cps2H; Xaa is a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
"Cps2D; encodes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
2. .721
/*tag= a
                                                                                                                              BP
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/note= "Cps2J; (
14574. .15578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note= "Cps2I;
3583. .14581
                                                                                                                              standard; DNA; 26281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3808. .12176
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/*tag= d
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The present sequence represents the capsular gene cluster of Streptococcus suis serotype 2. The genes in this cluster are involved in polysaccharide biosynthesis of capsular components and antigens. The proteins are involved in regulation (CpsB, CpsC, CpsC, captolation (CpsB, CpsC, CpsC, CpsC, and biosynthesis (CpsE, CpsC, CpsG, CpsG, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC, CpsC,
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P-PSDBB; AAYG8950, AAYG8951, AAYG8952, AAYG8953, AAYG8954, AAYG8955,
AAYG8956, AAYG8956, AAYG8958, AAYG8959, AAYG8960, AAYG8961, AAYG8962,
AAYG8963, AAYG8964, AAYG8965, AAYG8966, AAYG8967, AAYG8969, AAYG8969.
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17.1%; Score 1195.8; DB 3; 78.9%; Pred. No. 1.1e-151; ive 0; Mismatches 382;

Best Local Similarity 78.9 Matches 1437; Conservative

Query Match

DB 3; Length 26281;

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14481 CGICCICIGITITIAAAAGAATAIGTAAATTAATIGITIGCTAAIAATITIGITTAAAATTT 14540
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                                                                                                                                                              TCTTCAGATTCATCAACGGATATATGTTTGGAATACGCAGAGCAAGATGGTAGAAAAA 13762
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ATGGATAAAATTAGTGTTATTGTTCCAGTTTATAATGTAGATAAATATTTAAGTAGTTGT
                            13583 ATGGAAAAAGTCAGCATTATTGTACCTATTTTTAATACGGAAAAGTACTTAAGAGAGTGT
                                                                13643 Tragaraccarrarreccaarcgraracraarcraagagarrerrigaragargaeger
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CITITITIATIGGGAGAIAGITITIATCATIACGCGACGIGGGTIGGCATTATITACCATIC 6593
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TAAACTICGITTIGGIATACCTATITAACGTAATTATTAAGCAGTTAAGGATAGCTTTC 360
                                                                                                                                                                                                     nucleic acid fragments containing exopolysaccharide operon, useful for increasing exopolysacchride synthesis in lactic acid bacteria
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 17468 BP; 5871 A; 2455 C; 3307 G; 5835 T; 0 U; 0 Other;
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Pred. No. 1.9e-119;
0; Mismatches 729;
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                                                  (INRG ) INRA INST NAT RECH AGRONOMIQUE.
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AACATTACGATCTCAAACATCTTGTTTTCCGATTTTTGAAGTCATGGGTATTGATGTGAGTG

AGTITITAGACGTAAAGCAATTCGTTTCAGATTTTGAGTTGTTAGGTATTGATGTAAGCG

SUL S13	ccccus thermophilus. Location/Qualifiers 3421802 /*tag= a /product= "Transcriptional /hote= "The corresponding phown within the specificat 18032534 /*tag= b /product= "Polysaccharide peps13B protein" /note= "The corresponding phom within the specificat val start." 25433235 /*tag= b /product= "Polysaccharide peps13C protein" /hote= "The corresponding peps13C protein" /hote= "The corresponding peps13C protein" /hote= "The corresponding peps13C protein" /hote= "The corresponding peps13C protein" /hote= "The corresponding peps13C protein" /hote= "The corresponding peps03253985
61 TTGATATTAATTCATTCATTTACTGCGTTGAAAAACAAAAAAAA	TCTGTATTGGGGGAAAAAATGAAAATTTGTTTGGTGGGTG

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The invention relates to a novel strain of a lactic acid bacterium that are defined in the specification. The bacterium of the invention may be useful during food preparation, particularly that of beverages and meat, cereal, or dairy products e.g. fermented milk, yoghurt, 'matured' cream, dessert cream, cheese, soft cheese, cheese spreads, cottage cheese, milk-based drinks, dairy product retentates and baby milk, where the products are derived from an animal and/or plant. The current sequence is that of the Streptococcus thermophilus CNCM I-2980 polysaccharide synthesis-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 437 TGAATCACATAAACAAATTCAAAAAATCTTGTTGCATTGGTAGTTTTAGGTACAGAAAT 496
              /product= "Transposase IS1193 protein"
/note= "The corresponding protein sequence is not shown
shown within the specification"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5712 TGAGTCAGATCAACTTCCTATCAAATATTTGGCAGGTATAGTAGTCATCGGAGATGGTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5772 AGTGGCGTTTCCAGAGGAGTCCCAATAATTCCTTTT---GATGATGCGATTGACTTTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5592 ATACTITATICAÁCTGCACGTAGATACAAATATCTATTCCTTATGACTGCTGAACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5829 GACTCATGAAGTTGTCGACCATGTTTATCAACTTACCGAGTGAACATTACGATCTCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            617 GCAATTCGTTTCAGATTTTGAGTTGTTAGGTATTGATGTAAGCGTTGATATTAATTCATT
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                                                                                                                                                                                                                                                                                                                           New strain of lactic acid bacteria, useful for preparation of foods apharmaceuticals, especially fermented dairy products, contains genes involved in polysaccharide biosynthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 16032 BP; 5191 A; 2323 C; 3188 G; 5330 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                           Fremaux
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                                                                                                                                                                                                                                                                                                                                                                                                 5; SEQ ID NO 1; 35pp; French.
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                                                                                                                                                                                                                                                                                           WPI; 2004-671092/66.
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                                                                                     FR2852604-A1
                                                                                                                      24-SEP-2004
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/note= "The corresponding protein sequence is not shown
shown within the specification. The CDS has a prokaryotic
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/note= "The corresponding protein sequence is not shown
shown within the specification. The CDS has a prokaryotic
                                                                                                                                      sequence is not shown
he CDS has a prokaryotic
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note= "The corresponding protein sequence is not shown
hown within the specification"
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/note= "The corresponding protein sequence is not shown
shown within the specification"
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/note = "The corresponding protein sequence is not shown
shown within the specification"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'product= "Repetitive unit polymerase eps13L protein"
"note= "The corresponding protein sequence is not shown
shown within the specification"
   'product= "Polysaccharide polymerisation/export-related
                                                                                                                                                                                                                                                                                                                                                                               note= "The corresponding protein sequence is not shown shown within the specification"
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'product= "Undecaprenyl-phosphate glycosyltransferase
                                                                                                                                                                                                                        product= "Undecaprenyl-phosphate glycosyltransferase
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                                     /note= "The corresponding protein sequence is not
shown within the specification"
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/note= "The corresponding protein sequence is not
shown within the specification"
13049. .14482
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shown within the specification. No start codon."
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                                                                                                                   eps13E protein"
/note= "The corresponding protein se
shown within the specification. The
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                 ps13D protein"
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us polynucleotide SEQ 1527 ATTTTGCAT 132 || || || | ATATTGTCT 46443 ; Gaps 31;

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45512 GAUTOCCTGGTTGTGCANATACTGGTANATACTGTTCAGTTTGTGCACATACTTTANATACTG 45511 TANGTHE GAUTOCCTTACTGATACTTGTGCACATACTTANATACTGGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG
6 8 6 8 6 8 6 8 6 8 6 8 6 8 6 8 6 8 6 8
133 TITTANATCACGANTCCACTTCAANTTTCCACTTCAACCTCACTTCAACCTTCAACCTTTTTTTT

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3397 TAGTITTATTAGGTATATCTGCATTGTATTATTCAAAATGGGAAAGATATTGTATTTT 3456 43209 GTATCGAACCTATAAAAAAGAATTTACTATTGTAATAAAAAACTATTGCTC 43152 3457 TAGACGACCTTATAGGACTAGCTTATCTATTAACAGCGGTCAAACCAAACTAGTTGCTC 43152 43151 TGATATGGCAGGAGGAAGAAATGATACCTTATAACATTATTATTGTTGTTTT 3456 43151 TGATATGACGAGGAGGAAAATGATACCATAAAGTTATTGTTGTTGTTTT 43092 3517 GCTTTATGAACTATCCTACGTTAAATACCACTAAATTATATTATAGTTTCAATTCT 3576 43091 GGAGGAAATCCTTACCAAGATAATTATATATAAAAACTTGGAGAACAATGT 43032 3577 TTGCACTTATAAAAAAAAAAAAAAAAATGAAAATTTTTTTT	CCGGATTAIGAATTAITGAATGGAATGAGCATAATTATGATGT	TCTAGAGAATCAAGTAATTATTATTATCAAGGAAGTATTGATAAAGTA AGTTGTGATGAATACGAAGGTTAATTATTATTATCAAGGAAGTATTGATAAAGTA AGTTGTGAAAACGAATAATAATAATTAATTAATAAAGGCCTGTTAAAGGCACTCTTTTTAAAA TTAGAAAACAATATTTTATTT	42531 TIGATGATATAACAATAIATCGAGAAATTATTTAATCCAAAGAATTTATTAACAGGTA 42572 4056 GCACTATTTATATTTACCATCATTAGCCATATTTTTCATATAGAACAATGAAACAATAGAAAA 42512 42571 AGGTTGATTGTCTTTTCTTTTCTTATACCATTTACGAAAGAAA	GGTTATTCTCGTAAATGGAAGTACTGATGATTCTGAGAAATTTGCTTAAACTATAT GTTATCCTATC-TGTAATGGAAGTACTGATGATTCTGAGAAATTTGCTTAAACTATAT TTATCCTATC-TGTATGATTCTCTATGTAATCAAATAAAATTTTATATGGTTGAT GAAGAACGATGGAAGAATTAAATATTACAAGAAATTTATATGGATGG
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GAAGAATTTAAGGTAATATTAAAGGAGTTGTGCGATGAAAATCAATAAAAACTCTTTATT AGATGCATATTTGATAATGGCTTATCATAATTTTTCCAGATTTTACTGGAGGGAAACTC TTATATTGCAATATTTTTAGTTAATTTTTTTAAATCACTGGGTTTAGGCGAGGGAAACTC AGATATTATCATCTTCTCTCAGGAGAATGCACCACTAGTTCCTTCAGATACCTGTAT	2504 AAAGAAATATGAACGAGTTAAATGTTACAGATTATTCCTAATATCAGAA 2563 44082 TGATCATCTTTTATTATTATTATTATTATTATTTTTTTATTA	43921 AATGAATTTTGGGAAATTAGTAGAAATTAAGTATGTCAATTTTTATAGGGAT 43862 2744 AAAGGCTTATTTATTTAGTGAAATGTCAGAGGACGATTACAGGGAT 43862 2744 AAAAGGCTTATTTATTTAGTGAAATGTATTTGGTCATTTATAGAGAATTA 2803 43861 GGACAATTTATTCTGAAAGTGA-CTTAGGTTTTGGTCATCTAATTCATAGTTTT 43803 2804 TAGAAAATGAATTTTCAAATAGATTATTGTAAATAGAAATTTAAGATTATAA 2860	43682 GTATTATATCTAATTATTATTATTATTATTATGACAAAGATAGCTTAATAA 43623 2981 AATITAAAGAAATTATTATTATTATTATTATTATTATTAGCAGAATAAAA 43623 43622 AAGAGTATTTATGAAATTATTACAAAAATTATTATTATTATTAGTACTTATTATTAGTATTAT 43563 3037 TGTTTAAATTATTAAATATGACCCCAATGTACAATTTATTATTATTAGTACTTTTTA 3096 43562 GAGTTCTACAATTTTTAAATATCAAATTTTATTATTATTAATTATT	43442 TAAGGAACAAGTTTTTTTTTTTTTTTTTTTTTTTTTTTT

TATAGAAGTTGCAATGTTCGAGGAATGATAATATAACTGAGTATAATGCCGATAT TCTGCCAATGGCAATGTTCGAGGAATGATAATTATCTTTGTTTG	5196 CCAGTITATAATGTAGATAATTTAAGTAGAAAGCATTATTAATCAAAAT 255

ATTAATTCACAGTATTTAAAAAGAGATTAAAACTTTATACTTTAGAGGTGGCGTTGGAAGAA 11039 40396 40924 40864 10684 GATTTTAAATTATATGATACAGTTGATTATTACAGAAAAAAATATAGAAAATATTTTAAG 40625 6155 40276 0215 GATGCAATCGAGAGAATGGTTGAATTTAGCGAGAAATATAATTCAGAAATTTTTTAGGG 40156 10155 TGTTATGTTGAAAAAAGAGAACAACATATTATAAATATCGTTTTAGAAGATGAAATGATA 40096 10095 GAAACTATTAGTCCAGTACAAGCAATACAAATATTTATAA---TTATGATGCCTATAGA 40039 6035 6095 6275 6335 6395 6455 TT---CATCCAACGTTTACACGAAGCAATTGAGAGAGAGAATGCCCTTGTGGCCAGTTGCT 6512 CATCGCTTTGTGGTGGCCTGTAATAAACTCTATAAAAAAGAACTATTTGAAGATTTTCGA 6686 6096 ATAAGAATTGTTTCGAACAAAGTTTTTAAAAAAATATTATGGTTATAATAGGAAGATATC CGCATTCGTTATTTTAAAAAGAGAACGCCGGGCTATCAGATGCCCGTAATTATGGCATA Argrafianggahancriargangrinccccgitagcah----antratarccahan 10863 ATTTTAGCGATAATAGTACTACTAGGACAAAATTCAATGAGAGAATGT-TGTATTTTTTT TTGGAAAATTTGCAAAAACAAGTGATAGTATTGTTTAAGCAAATATATGTGAGGATTTT AAAAATTTTATGAATTTGTATAAATAATATTTTTTTTTCTACTCCTGTTTGTAAACTATAT AAGAAAAGATACATAAACAGATCTTTTTCAAGAGAATCAATGGTTAGGAGAAGATTTACTT GTAATTTATTGAGTAATCCATATCCAGAAGGAAAATTCATGAAGATATGGATACAACTT Traagcerratargcecercaaaaaragcagerrigegararrecacegegerer TTTTATAGGAGAGGTATACTAAGTACAGTAAATTCTTTTAAAGAAGGTGTGTTTTTGCAA GACGTATCAATTGTTAAAGATACTATACGTTGGCAAGTATTTTATTATAATGCTTACTAATG 10564 TCCTCTATAAGATATTTCACTATTGTAAGAAAATA-----TATAATTTGAGGTTATC 6156 ATGGATACTATTAGTAAATTTCTATAATTGTACCTATATAAATGTAGAAAAATATTTA 6216 TCTAAATGTATAGATAGCATTGTAAATCAGACCTACAAACATATAGAGATTCTTCTGGTG 10455 AACGAGTGTATAGAAAGTGTTTTAGGCTCAAACTTATTCAAATTTAGAAATTATTCTAGTT AATGACGGTAGTACGGATAATTCGGAAGAATTTGTTTAGCATATGCGAAGAAGATAGT GGTTATG-----ATAGGGTAGATGCTTCGGGGCATTTCTTAACAGCAGAGCCGCTTCCT 5976 TTTAAATACGGAAAACAGTCTATTTTGACAAATTTTTAATTTTTTAGAAATCTTTATAAA AAATATTTTTTAACTTGTTAAAAGTATCTAACAAAAATTCTTTGTCTAAAAATTTTTGT 6567 ACAAATCAGGCTGTTCTGAGCGGCAGGAATGTTTGTAAAAAGCTGCTAGAGGCGGATGGT 9699 40983 9169 6276 6336 5736 40923 5796 5856 6456 6036

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1995 ATGTAGAGGCACTTAGCTTTGATAATATAGGAGAAAAGCGAATCCAAACTTTTGAAGGAT 1154
                                         The invention relates to a protein having betal,3-galactose transferase activity, derived from a microbe having an activity of transferring galactose to N-acetyglucosamine by betal,3-bond. The protein can be used in a method for the preparation of a protein having betal,3-galactose transferase activity in which the above transformant is cultured in a medium to form and accumulate a protein having betal,3-galactose transferase activity, and in a method for the preparation of a galactose containing gluside in which a culture liquid of the above transformant or a treated product of the culture liquid of the above transformant or a treated product of the culture liquid of the above transformant or made to be present in an aqueous medium, and a galactose-containing gluside is formed and accumulated in the aqueous medium. The galactose-containing gluside is used as a candidate for infection preventors. This sequence represents DNA encoding betal,3-galactose transferase proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      975 AGTTAACCTGCTTAACTGTTGATCAAGCTTTTATTAACATACCCATTGAATTATTTGGTA 1034
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          553 TTTCAACAAGGGAAGTGGTCGACCACGTCTTTATAAATCTACCAAGTGAGTTTTTAGACG 612
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   373 TCTATCAAAAAAGACGATTCTAATTACAACGGCTGAACGATGGGAAAATATGCAAGTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              433 TATTTGAATCACATAAACAAATTCAAAAAACTTGTTGCATTGGTAGTTTTAGGTACAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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Pred. No. 6.9e-89;
       Example 1; Page 15-22; 24pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10.4%;
59.2%;
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40038 GCTATTTTACTGTAGCACATAATTATATAAAGAGAGAATTATTTTCTACGCTGTGC 39979
                                                                                             TATCCAGTAGGGAAGTTACACGAAGATGAATTTTTAACCTATAAATTATATTTGAAAGCC 39919
                                                                                                                                                                                      9918 AAAAATATAATTTTCTTTAGATATAATACTTATGCATATCGTATTAGAGAAAATAGCATA 39859
                                                 TTTGAAAAGGGTAAGATTCATGAAGATGAATACTTCACTTATCGCTTGCTCTATGAGTTA 6746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Betal, 3-galactose transferase; gene; ds; galactose; N-acetylglucosamine; betal, 3-bond; galactose-containing gluside; uridine-5'-diphosphate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Betal, 3-galactose transferase and a DNA encoding the enzyme, a protein having betal, 3-galactose transferase activity, a transformant, preparation of a protein, and preparation of a galactose-containing gluside.
                                                                                                                                          6747 GAAAAAGTTGCAATAGTTAAGGAGTGCTTGTACTATTATGTTGACCGAGAAAATAGTATC
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                                                                                                                                                                                                                                                                                    Argaciegirccracariarraaaaggcracargcrgragaaggacrraa 39809
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product= "Betal,3-galactose
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2265. .2747
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Superantigen; ds; gene; SAg; staphylococcal enterotoxin; tumour; cancer; apoptosis; gene therapy; mammalian cell receptor; cytostatic; tumour associated lipid; anergy; T cell; antigen presenting cell; APC; tumouricidal immunocyte; antitumour.
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                                                 TATAAAAAATTTCTCAGTTACAAAGAAATGGAACAATATATTAACAAATCAGAAGTAGTT
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                                                                                                    TAGTTCCAATTATTCGTAGAGGTGGACCGGCTATTTTTCCTCAGAAACGAGTTGGAC
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cellular inactivation or geath is deleted or functionally deactivated, producing (M1) a tumouricidal immunocyte population in vivo in a mammal by allowing tumour associated lipids to contact immunocytes in which receptors for immunosuppressive fatty acids, ceranides, gangliosides, sialylated glycans, lipopeptides and proteoglycolipids are inactivated or deleted, a construct useful in the treatment of cancer comprising a capture of SAB) nucleotide inserted into a virus, a mammalian T cell useful in the treatment of cancer comprising a compressing a lipid raft conjugated to a superantigen, which the treatment of cancer (where an adaptor protein, which cancer (comprising a lipid raft conjugated to a superantigen), producing (M2) a tumouricidal immunocyte population ex vivo in a mammal (by allowing tumour associated lipids to contact immunocytes, in which receptors for the tumour associated lipids are inactivated or deleted to produce a cutvated immunocytes population, and administering the tumouricidal APC contact APCs, in which receptors for the tumour associated lipids are inactivated or deleted to produce a tumouricidal and administering a tumouricidal by allowing a tumour associated lipids are inactivated or deleted or produce a tumouricidally activated population, or a mammal (by allowing a tumour associated lipids to contact APCs, in which receptors for the tumour associated lipids to contact T cells, in which adaptor proteins, which inhibit T cell or activated to produce a tumouricidal population of T cells, and administering the tumouricidally activated T cells to the host), treating deactivated to produce a tumouricidal population of T cells, and administering the tumouricidally activated T cells to the host), treating (M5) cancer in a mammal Boy administering a lipid and antigens, are deleted or functionally activated T cells to the host), treating to binds immunosuppressive tumour associated lipids in vivo in a mammal C cumour associated antigen to contact T cells averaged antigen to contact mammala con The invention relates to a mammalian cell receptor, useful in the treatment of cancer, which binds to tumour associated lipids and induces anergy or apoptosis in the T cells and antigen presenting cells (APCs). Also included are a mammalian cell useful in the treatment of cancer where the receptor which binds tumour associated lipids and induces cellular inactivation or death is deleted or functionally deactivated, tumouricidal T cell population ex vivo in a mammal comprising allowing a sequence encodes an anti-tumour protein which is co-administered with or superantigen-lipid raft conjugate to contact immunocytes in vivo. The receptors, methods and compositions are useful for treating cancers and tumours. Bacterial superantigens are co-administered or administered as specification, but was obtained in electronic format from the US patnet office website at "segdata.uspto.gov/sequence.html?bocID=20020177551" incorporated into a fusion construct with a superantigen. Note: The sequence data for this patent did not form part of the printed The present fusion constructs with anti-tumour proteins or motifs. Example 2; Page; 167pp; English

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9 CICCCCAATTTTAAAAGCAATAAAGATTTATTGTTTGTTCTATTGATACATTATATTGTTT 4884 TTTTTATATATCTCGTATGCCAGTTGAATTTGAGTATAGAGGTAATCTGATAGAGTTTGAAA 192 TGGCATTATTTGATATGATAGCAGTTGCAATTTTCTGCAATCTTAACAAGTCATATACCAA 76 AIGCIGALTTAAAICG---ITCIGGAATTTTTAICATAAIGAIGGITCAITAITTTGCAI Gaps Sequence 17276 BP; 5953 A; 2414 C; 3043 G; 5866 T; 0 U; 0 Other; 38; 0; Mismatches 902; Indels DB 8; Score 726.8; DB Pred. No. 9e-89; 10.4%; 59.2%; Matches 1366; Conservative Similarity 16 4765 4825 133 Query Match

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4885 TTTATCTTTCTGATTTTTACAGAGACTTTTTGGAGTCGTGGCTATCTTGAAGAGTTTAAAA 4944

193 AAACATTTAACTATAGTATAATATTTGCAATTTTTTTTTACGGCAGTATCATTTTTGTTGG 252

1143 5895 TTCGGTTGGACTTAGCATACATTGATAATTGGACTATCTGGTCAGATATTAAAATTTTAT 1323 GGATTACAGGTCTCTGGCAGGTTAGTGGTCGTAGTAATATCACAGACTTCGACGACGTAG 1263 ATGTAGAGGCACTTAGCTTTGATAATATAGGAGAAAAGCGAATCCAAACTTTTGAAGGAT 5481 492 s185 ggaaraaar---acgaccaraarrararcgcrercrerarriggacrecrergaaage 5241 5242 ATTGTTATGATTTGAAACATAACTCGTTAAGGATAATAAACAAAGATGCTCTTACTTCAG 5301 3302 AGTTAACCTGCTTAACTGTTGATCAAGCTTTTATTAACATACCCATTGAATTATTTGGTA 5361 3362 AATACCAAATACAAGATATTATTAATGACATTGAAGCAATGGGAGTGATTGTCAATGTTA 5421 ATAGTGTTATTACATATTCTATGAATTCTATAAATATAGTCACCTTATAGCAAAACGAT 5541 TTTTGGATATCACGGGTGCTATTATAGGTTTGCTCATATGTGGCATTGTGGCAATTTTTC 5601 racriccecaaarcaaaadarcereeccacrarcrirrcrcaaaaracacragerc 5661 s662 graatggraggattritagattcrataaattcagatcaatgcgagtagatgcagaacaaa 5721 TGGTATACCTATTTAACGTAATTATTAAGCAGTTTAAGGATAGCTTTCTATTTTCGACAA 372 663 TITIGGATATACTCGGAGCGGTAGTCGGGTTAATTATTTGTGGTATAGTTTCTATTTTGT 843 ATATTAATTCATTCGGTTTTACTGCGTTGAAAAACAAAAAATCCAACTGCTAGGTGACC 723 TAGITCCAATTATTCGTAGAGATGGTGGACCGGCTATTTTTGCTCAGAAACGAGTTGGAC 903 ----CTAATGTTTAAGTTAGA TACCACAGTITITATAATGTTTTAATTGGCGATATGAGTCTAGTTGGTACACGTCCACCTA recercaarreraargrirrraaaagecearareagrirraecageaacacecerecea CAGITGATGAATTTGAAAATATACTCCTGGTCAAAAGAGACGATTGAGTTTTAAAACCAG cactricaticaataticaaagtataatricaacgcagaagcgacgccttagtrittaagccag TATTATATATCTATTGAATTCATTTTTAAAATATTATCGAAAATATTCTTACGCTAAGTTTT TTTCAACAAGGGAAGTGGTCGACCACGTCTTTATAAATCTACCAAGTGAGTTTTTTAGACG **ATAGCATTGTAACTTTTTCCACAAATTTTTTATAAGCCTAGTCATATCATGATGAAACGAC** AAACGATCCTAGAATTACTCCAATTGGACATTCATACGCAAAAACAAGTTTAGACGAGT 5777 AGATGATCCTAGAATTACTAAATAGGAAAATTTATTCG-AAAAACAAGCATAGATGAGT AGAATAATTTCGCACTTTCAAGACGTGGTGCCGTGTATTTCACATTAATAAACTTCGTTT <u>aaaacrerirracaacaacacacrirrecrrrrrracrirrarracrargaarregarirr</u> 373 TCTATCAAAAAAGACGATTCTAATTACAACGGCTGAACGATGGGAAAATATGCAAGTTT 5125 CACGAGATACCAAAGTTGTTTTGATAACGAATAAGGATTCTTTATCAAAAATGACCTTTA 433 IATTTGAATCACAIAAACAAATTCAAAAAATCTTGTTGCATTGGTAGTTTTAGGTACAG AAATAGATAAAATTTAATTTATCATTACCGCTCTATTATTCTGTGGAAGAAGCTATAGAGT TAAAGCAA-----TTCGTTTCAGATTTTGAGTTGTTAGGTATTGATGTAAGCGTTG TTAAGAAAGATTTATTAGTTCACAATCAAATGACAGGG-313 5896 493 613 664 5422 724 5482 784 5542 844 5602 964 5722 1084 5836 1144 1204 1264

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                                                                                                  GAATATAATGAAATTTGTCTGGTTGGTTCAAGTGGTCGTCATCTAGCACACTTGAACCT
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                        AGATTAAAACAAATAGTTGAAAATT
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regular activation by receptors specific for lipid-based tumour associated antigen. The receptor has cytostatic and antimicrobial properties and is suitable for use in gene therapy. The receptors, methods and compositions are useful for treating a neoplastic disease or tumour (cancer), and infectious diseases. This sequence represents a moiety, the DNA of which can be transfected into a cell surface moiety, the DNA of which can be transfected into a cell with superantigen DNA to generate antitumour immunity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New receptor in a mammalian cell that inhibits regular activation by receptors specific for lipid-based tumor associated antigens, useful treating a neoplastic disease or tumor, and infectious diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           invention describes a receptor in a mammalian cell that inhibits
                                                                                                                                                                                     cytostatic;
tumour; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 17276;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 17276 BP; 5953 A; 2414 C; 3043 G; 5866 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                38;
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disease;
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Pred. No. 9e-89;
0; Mismatches 902;
                                                                                                                         Sterptococcus capsular polysaccharide DNA seg id
                                                                                                                                                                        receptor; lipid-based tumour associated antigen antimicrobial; gene therapy; neoplastic disease infectious disease; capsular polysaccharide; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 3; SEQ ID NO 83; 151pp; English
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Matches 1366; Conservative
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1546 6315 6375 1666 6435 1726 6495 1786 2146 6255 1606 1906 6675 2026 6795 2086 GTTGTTCCTAGGAGAAGCAGTTTGGTGAACATATCAATGATCATCAAATACAATTTTTA 6915 6975 7035 7 AGAAGAATTTTACAAGATAATAATATTTTATTAGAAAATATAGATGATTTTGTTTGAA 2206 ATCACACATGGCGCCCCAGCGACGTTTATGTCAGTTATTTCTTTAGGGAAATTACCAGTT 6855 ATAACCGACGAATATTTATTCAAACAGGATATTCTGACTATATTCCAGAATATTGCAAG TTTGAAACCCATTTGGGAAAAAGAAGATGGTTTTGGGTAACCTTTGATAAAGAAGATGC TTGTTTCCTAGACAAAAAGTATGGTGAACATGTAAATGATCATCAAGTAGAGTTTGTA GTTAAAACCGTTTTGGAAGGAAGAAGAACGTTTTTGGGTAACATTTGATAAAGAGGATGC CATTAATTTAGTGAAAAATACTTTCTTAGCTTTCAAAATTTTTACGTGATGAGAAACCAGA TGTTATTATTTCATCTGGTGCGGCCGTTGCTGTCCCCTTCTTTTACATCGGAAAACTATT TGGAGCAAAGACGATTTATATTTGAAGTATTTGATCGAGTTAATAAATCTACATTAACTGG cargaacagcagricaaccgrcrrarraaagaagrigaragarraaaagggacaggrgcr TATAAAAAATTTCTCAGTTACAAAGAAATGGAACAATATATTAACAAATCAGAAGTAGTT Streptococci; GBS; capsular polysaccharide synthesis; cps; actiae capsular polysaccharide synthesis (cps) gene 7 AGATTAAAACAAATAGTTGAAAATT 2292 BP standard; DNA; 25020 2004 (first entry) 9 7 9 ~ 7 9 7 ø 9 7 9 9

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1263 GTTCGGTTGGACTTAGCATACATTGATAATTGGACTATCTGGTCAGATATTAAAATTTTA 1322
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                                                                                                 5514 TCACGAGATACCAAAGTTGTTTTGATAACGAATAAGGATTCTTTATCAAAATGACCTTT
                                                                                                                                                                                      GAAATAGATAAAATTAATTTTATCATTACCGCTCTATTATTCTGTGGAAGAAGCTATAGAG
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                                           5454 TTATTGTÁTCTÁTTGÁATTCÁTTTTTAÁAATÁTTATCGAAAATATTCTTACGCTAAGTTT
                                                                                                                             TTATTTGAATCACATAAACAAATTCAAAAAATCTTGTTGCATTGGTAGTTTTAGGTACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to compositions and methods for detecting group B Streptococci (GBS) Streptococcus agalactiae capsular polysaccharide synthesis (cps) gene in sample. The invention is useful for detecting S. agalactiae in a sample. The present sequence is S. agalactiae cps gene. This sequence is used to illustrate the method of the invention.
                                                                                                  specific probe"
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B Streptococcus cpsD-cdsE-cpsF-cpsG partial

(first entry)

03-JUN-2004

Group group

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cpal DNA

cpsF; cpsG; consensus

bacterium; cpsD; cpsE;

GBS

coup B streptococcus; gene; GBS infection;

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Streptococcus sp. WO2003025216-A1 SERVICE.

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This invention relates to a novel method of typing a group B streptococcus (GBS) bacterium which comprises analysing the nucleotide sequence of one or more regions within the cpsb, cpsE, cpsE, cpsE and/or cpsl/M genes of the bacterium, where the regions comprise one or more nucleotides having sequences that vary between types. The method is useful for preparing a composition for serotyping and/or subtyping a GBS bacterium for diagnosing GBS infections in pregnant women, elderly and/or immunocompromised patients. The present sequence is that of a consensus DNA sequence for the 3' and of the cpsD-cpsE-cpsE and the 5' end of the cpsC sequences of group B Streptococci which is related to the method of
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                                                                                                                                                                                                                                                                                                                                                                              Typing a group B streptococcus (GBS) bacterium for diagnosing the GB infections in pregnant women, elderly or immunocompromised patients analyzing the sequence of the regions in the cpsD, cpsE, cpsF, cpsG cps1/M gene of the bacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 11; Length 2226;
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llarity 59.5%; Pred. No. 2.5e-78;
Conservative 0; Mismatches 793;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence represents a fragment of the EPS plasmid derived from L. lactis subspecies cremoris Ropy352. The EPS plasmid is about 32 kb in size and encodes at least 13 active genes allow the bacteria to produce an exopolysaccharide, designated genes allow the bacteria to produce an exopolysaccharide, designated EPS352. When EPS352 is expressed in or added to milk, it imparts highly desirable sensory characteristics to the milk, including making the milk very thick, with a very smooth mouth-feel, and slightly sweet with an obvious chewable-bite. Open reading frames (ORF's) M and N show homology or oflycosyltransferase involved in EPS352 biosynthesis. L. lactis accession number NRRL B-30229. EPS352 biosynthesis. L. lactis accession number NRRL B-30229. EPS352 is useful for thickening a liquid selected from milk, a milk-based liquid, a an additive in pharmaceutical products, beauty care products and coating agents. It is pharmaceutically in the specification that there is an additional ORF between those encoding EpsE and Eps0. This encodes EpsF (AAB47425). However, this ORF is not indicated on the actual DNA sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New bacterium useful in pharmaceutical formulations, food products and beauty cosmetics, comprises characteristics of Lactococcus lactis cremoris Ropy 352.
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AAB47422, AAB47423, AAB47424.
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Similarity 58.9%; Pred. No. 9.6e-49;
49; Conservative 0; Mismatches 581; Indels 12;
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981 AGCCAAAACCAGATGCAAGGGTGGGTATGTTTTAAAATGGGAAAAACGATCCTAGAATTA 1040
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  CATTATCCAAAGGAAAAAACAATTATTGTTTCCTAGACAAAAAAAGTATGGTGAACATG
                      TATTACAACTAGGTAAATTCCGATAGTTCTTCCACGGCAAATGAAATTTGATGAGCATA
                                             TAAATGATCATCAA-GTAGAGTTTGTAAGAAGAATTTTACAAGATAATAATATTTTATTT
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antibacterial; drug design.
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23-OCT-2000; 2000US-0242578P.
27-NOV-2000; 2000US-0253625P.
22-DEC-2000; 2000US-0257931P.
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be used to screen compounds in rational drug discovery programmes. The antiense mucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence encodes an essential prokaryotic cellular proliferation protein. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the true of the printed specification.
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Pred. No. 5.1e-48;
0; Mismatches 548; Indels
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58.6%;
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Matches 794; Conservative
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                                                                                                                                                                                         TITATGGCAGGTCAGCGGACGAAGTGAGATCAAGAATTTCGATGAAGTTGTCAAATTAGA 1274
GATTCGAAAGGATGGGGGATCTGCTATTTTTGCTCAGACGCGTATAGGAAAAATGGTCG 920
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                                   rcagricacrirriaraagriricecrcrargrergragargccgaggcgaaaaaaagaga
                                                                     ACTCATGGAACAAAATACCATGCAAGGTGGAATGTTT----AAGGTGGACGATGATCCT
                                                                                                         CETATCACGAAAATTGGTTGTTTATACG-GAAGACTAGCTTGGACGACGACTT
                                                                                                                                 TTATAATGTTTTAATTGGCGATATGAGTCTAGTTGGTACACGTCCACCTACAGTTGATGA
                                                                                                                                                                                                           TCTCTGGCAGGTTAGTGGTCGTAGTAATATCACAGACTTCGACGACGTAGTTCGGTTGGA
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                 CTTGCTCAGCCAAAACCAGATGCAAGGGTGGGTATGTTTTAAAATGGGAAAAACGATCCT
                                                                                            AGAATTACTCCAATTGGACATTTCATACGCAAAAACAAGTTTAGACGAGTTACCACAGTT
                                                                                                                                                  TTATAATGTTCTAAAGGGAGATATGAGTTTGGTTGGCACACGGCCACCAACACAGGGCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              useful for diagnosing, preventing and/or treating conditions resulting from the bacterial infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated nucleic acid encoding a Streptococcus pneumoniae
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                                                                                                                                                                                                                                                                                                                                                                                                                                   bacteraemia; pneumonia; otitis media;
                                                                                                                                                                                                                                                                                                  1335 TAAAGTAGTATTTATGAGAGATGAGGAGGAGTAA 1368
                                                                                                                                                                                                                                                                                      GAAAGTTGTATTGTTGAGAGGGAAGTAAGTAA 1367
                                                                                                                                                                                                                                                                                                                                                                                                                S. pneumoniae DNA sequence, SEQ ID 2303
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                                                                                                                                                                                                                                                                                                                                                        ADR93668 standard; DNA; 1443 BP
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pathological
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cc fragments, with any of 9 fully defined sequences (appearing as ADR94308, ADR94899, ADR95423, ADR95642, ADR95642, ADR95642, ADR95642, ADR95642, ADR95642, ADR95642, ADR95642, ADR966079) or any of the fully defined sequences appearing as ADR91705, ADR91886, ADR92197, ADR92234, ADR93039, ADR93079, ADR92366, ADR92650 or ADR991886, ADR92197, ADR92234, ADR93039, ADR93079, ADR92366, ADR92650 or CC ADR99476 or at least 40, 60 or 30 consecutive mucleotides of the nucleotide sequence. Sequences, or at least 40, 60 or 300 consecutive mucleotide sequence. CC red nucleic acids and proteins are chosen from $206 disclosed sequences. CC Also included are a recombinant expression vector comprising the isolated nucleic acid cited above operably linked to a transcription regulatory comprising at least 20 consecutive nucleotides of the nucleotide sequences as cited above. The methods and compositions of the present sequences as cited above. The methods and compositions of the present invention are useful for the diagnosis, prevention and/or treatment of pathological conditions resulting from bacteraemia, meningitis and citis media. The present sequence is one of the 2603 disclosed S. CC patenn did not form part of the printed specification, but was obtained correct or sequence. The pathological conditions to the printed specification, but was obtained correct conditions to the printed specification, but was obtained correct conditions to the printed specification, but was obtained correct conditions to the printed specification, but was obtained correct conditions to the printed specification, but was obtained correct conditions to the printed specification, but was obtained correct conditions to the printed specification, but was obtained correct conditions to the printed specification, but was obtained correct conditions to the printed specification.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              434 ATTIGAATCACATAAACAAATICAAAAAATCITGITGCATTGGTAGTTTTAGGTACAGA 493
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1443;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1443 BP; 432 A; 218 C; 340 G; 453 T; 0 U; 0 Other;
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CIE DANONE SA GERVAIS RHODIA CHIM.

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                                                                                                ACTCGGAGCGGTAGTCGGGTTAATTATTTGTGGTATAGTTTCTATTTTGTTAGTTCCAAT
                                                                                                                       TATCGGTTCCCTGGTAGGTTTGATACTATGTGGTCTAGTCAGTATTGTACTGGTTCCTTT
                                                                                                                                                TATTCGTAGAGATGGTGGACCGGCTATTTTTGCTCAGAAACGAGTTGGACAGAATGGACG
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ATTCGGTTTTACTGCGTTGAAAAAAAAAAAAATCCAACTGCTAGGTGACCATAGCATTGT
               TTTCGATTGTATCTTGGCACATAACAAATTTGTGAGATGGCAGGACTAAACGTTGT
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                                                                                                                                                                                                            Proteins encoded by the eps operon function in exopolysaccharide (BPS) synthesis. The operon is useful for producing chimeric eps operons, for optimising production of BPS in lactic acid bacteria. BPS impart texture, mouth feel and rheological properties to fermented food products (e.g. yoghurt). They function as thickeners, to provide free-flowing and creamy texture, and may also have biological activities beneficial to health
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   312
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                                                                                                               nucleic acid fragments containing exopolysaccharide operon, useful for increasing exopolysacchride synthesis in lactic acid bacteria.
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                                                                                                                                                                                                                                                                                                                                      Sequence 18274 BP; 5799 A; 2843 C; 3571 G; 6061 T; 0 U; 0 Other;
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                                               Renault
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                                               Mengand
                                                                                                                                                                                                                                                                                                                                                                      Score 383.2; DB 6;
Pred. No. 1.1e-42;
0; Mismatches 578;
                                             Fremaux C,
                                                                                                                                                                  Claim 9; Page 104-109; 144pp; French
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llarity 56.6%;
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/note= "encodes AAY43773; this CDS, minus the termination codon, is specifically claimed (claim 6)"
12838. .13788
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDS, minus the termination (claim 6)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "encodes AAY43776; this CDS, minus the termination codon, is specifically claimed (claim 6)"
                                                                                                                                                                                                                                       /product= "eps6; this CDS, minus the termination codon, is specifically claimed (claim 6)"
//note= "encodes AAY43772; contains a stop codon at nucleorides 9410-9412"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New recombinant enzymes for biosynthesis of exopolysaccharides having e.g. antitumor or probiotic properties or useful in fermented milk products.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product= "eps9"
/note= "encodes AAY43775; this CDS is specifically
                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "encodes AAY43774; this codon, is specifically claimed 14138. 15553
                                                                                                                                                                        'product= "eps5"
'note= "encodes AAY43771"
j633. .10681
                                 /product= "eps3"
/note= "encodes AAY43769"
                                                                                                                        "encodes AAY43770"
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AAX43773, AAY43774, AAY43775, AAY43776.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Germond JE, Lamothe G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 6; Page 77-97; 163pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (claim 6)"
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/product= "eps7"
                                                                                                     product= "eps4"
                                                                                                                                                                                                                                                                                                                                                                                                                                              'product= "eps8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16919. .18016
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/product='
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22-APR-1998;
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1032
                                                                                                                                                                                                                                                                                                                                  AATTGATGGATAAAATCAAATGTCTGGTGGTATGTTT----AAGATAGACAATGATCC 5599
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                                                                                                                                                                                                                                                                                                                                                                                                            5658
                                                                                                                                                                          TITATAATGITITAATIGGCGATATGAGTCTAGITGGTACACGTCCACCTACAGTTGATG 1152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AATITGAAAAATATACTCCTGGTCAAAAGAGACGATTGAGTTTTAAACCAGGGATTACAG 1212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTCTCTGGCAGGTTAGTGGTCGTAGTAATATCACAGACTTCGACGACGTAGTTCGGTTGG 1272
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1273 ACTIAGCATACATIGATAATIGGACTAICIGGICAGATATIAAAAATITIAATAAAGACAG 1332
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                                              5305 Trangriticiracscartitrarasarargasgararciticscoaaacscriccrosara 5364
                                                                                                                    TCTGCGGAGCTCTAGTTGGTTGTTGCTCTGTGGTATTGTAGGAATCTTCCTTTATCCTC 5424
                                                                                                                                                                                                                            GCATATTTACATTCTACAAGTTTCGATCGATGTATGTTGATGCTGAGGGGGGCGCAAAAAG 972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         eps3;
            TAACTITITICCACAAATITITIATAAGCCTAGTCATATCATGATGAAACGACTTTTGGATA
                                                                                 TACTCGGAGCGGTAGTCGGGTTAATTATTTGTGGTATAGTTTCTATTTTGTTAGTTCCAA
                                                                                                                                                      TTATTCGTAGAGATGGTGGACCGGCTATTTTGCTCAGAAACGAGTTGGACAGAATGGAC
                                                                                                                                                                                                                                                                                                 973 ACTIGCICAGCCAAAACCAGAIGCAAGGGIGGGIAIGITITAAAAIGGGAAAAACGAICC
                                                                                                                                                                                                                                                                                                                                                                                               5600 ACGTATTACCAAGATTGGACATTTCATTCG-TAAAACAAGTCTTGATGAACTTCCACAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          eps operon; Streptococcus thermophilus Sfi39; enzyme; eps1; eps2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    eps4; eps5; eps6; eps7; eps8; eps9; eps10; exopolysaccharide biosynthesis; EPS; intersugar bond; antitumour; probiotic; foodstuff; organoleptic quality; flavour; lactic acid bacteria; acidified milk product; yoghurt; cheese; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGAAAGTTGTATTGAGAGGGGAAGTAAGTAAAAGTATATGAAAGTTTGTT
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/product= "eps2"
/note= "encodes AAY43768"
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3390. .4121
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6830 1201

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1381 7010

EPS6;

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6711 ACTICCACAATITIGGAAIGTICTAAAAGGIGATAIGAGCTIGGTIGGGACACGICCTCC
        AATCAAGAAGAATTTGATGGCACAGAATCAAATGTCTGGTGGTATGTTT-----AAGATG
                                                                                                                                                                         1022 AAAAACGATCCTAGAATTACTCCAATTGGACATTTCATACGCAAAAACAAGTTTAGACGA
                                                                                                                                                                                                                             GACAATGATCCACGTATTACCAAAATTGGACATTTCATTCG-TAAAACGAGTCTTGATGA
                                                                                                                                                                                                                                                                                     GTTACCACAGTTTTATATGTTTTAATTGGCGATATGAGTCTAGTTGGTACACGTCCACC
                                                                                                                                                                                                                                                                                                                                                                                                 TACAGITGATGAATTTTGAAAATATATACTCCTGGTCAAAAGAGACGATTTGAGTTTTAAAACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                        6771 AACAGTTGATGAGTATGAAAAATATACACCTGAACAGAAACGTCGTTTAAGTTTTAAACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1202 AGGGATTACAGGTCTCTGGCAGGTTAGTGGTCGTAGTAATATCACAGACTTCGACGACGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6951 ATTGAAAACGATTAAAGTAGTAGTAATGAAGGATGGAGCAAAGTGATGGCTTTCACCATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Exopolysaccharide; EPS; ESP enzyme; EPS1; EPS2; EPS3; EPS4; EPS5; EPS6
EPS7; EPS8; EPS9; EPS10; Streptococcus thermophilus strain Sfi39;
activated D-galactose pyranose; saccharide; beta-glycosyltransferase;
transporter; food; fermented milk product; yoghurt; cheese;
flavour stability; organoleptic property; ss.
                                                             AGTTCGGTTGGACTTAGCATACATTGATAATTGGACTATCTGGTCAGATATTAAAATTTT
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note= "encodes AAY54066"
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/product= "EPS5"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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used in foodstuffs to improve organoleptic qualities and flavour. When expressed by lactic acid bacteria, EPS impart a free-flowing character and/or a smooth, creamy texture to acidified milk products (yoghurt or
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2 TCGCCAAACGAAATTGGCATTATTTGATATGATAGCAGTTGCAATTTCTGCAATCTTAAC

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The present sequence encodes enzymes involved in the biosynthesis of exopolysaccharides (EPS). These enzymes are designated EPS1-EPS10. and are encoded by open reading frames eps1-eps10. The enzymes are isolated from Streptococcus thermophilus strain Si139. The proteins are used in a method for the synthesis of EPS, which includes at least one step of forming a bond (alpha or beta-isomer) between C-1 (carrying the reducing aldehyde function, of an activated D-galactose pyranose), and a phosphate on a lipophilic or proteinaceous primer. Stepwise synthesis of EPS occurs with, in each step, addition of a new sugar unit, through its hemi-acetyl function, to an alcoholic hydroxyl of a second sugar unit, present at the cond of a chain of sugar residues bonded to the primer. EPS1 to EPS4 are used to elongate the EPS chain, and to regulate EPS production, EPS5 creates new bonds between saccharides, EPS6 is used in the biosynthesis of EPS, EPS7 and EPS8 are beta-glycosyltransferases, EPS9 is a transporter of repetitive units, and EPS10 catalyses the conversion of a pyranose form of a beta-D-galactose to the furanose form. The EPS enzyme or properties of foods, particularly fermented milk proporties.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New recombinant enzymes for synthesis of exopolysaccharides, particularly in lactic acid bacteria, for improving properties of fermented milk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                products such as yoghurt and cheese, e.g. their organoleptic properties and flavour stability
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY54068, AAY54069, AAY54070
                                                            /note= "encodes AAY54070; contains 1 stop codon nucleotides 9410-9412"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 19966 BP; 6405 A; 3134 C; 3732 G; 6694 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                 /*tag= j
/product= "EPS10"
/note= "encodes AAY54074"
"encodes AAY54069"
                                                                                                                                              /note= "encodes AAY54071"
12838. .13788
                                                                                                                                                                                                                                                                                /note= "encodes AAY54073"
16919. .18016
                                                                                                                                                                                                               /note= "encodes AAY54072"
14138. .15553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P-PSDB; AAYS4065, AAYS4066, AAXS4067, A
AAYS4071, AAYS4072, AAYS4073, AAYS4074.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Germond JE, Lamothe G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 6; Page 77-96; 162pp; French
                                                                                                                                                                                                                                                               'product= "EPS9"
                                                product= "EPS6"
                                                                                                                                "EPS7"
                                                                                                                                                                                                 "EPS8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98EP-00201310.
98EP-00201311.
98EP-00201312.
                                                                                                .0703. .11671
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22-APR-1998;
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                                                                          62 AAGTCATATACCAAATGCTGATTTAAATCGTTCTGGAATTTTTATCATAATGATGGTTCA 121
                                                                                                                                                                                                                                                                                                       5769 TGTAGTGTCTTACTATATCAGTAGTTATTATGAAAATCTTAAGTATAGAGGCTACTTGGA
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5649 TCGTCGCATTGAAATTGGTATTATACAGTTGGTTGTGGTTGTTTTCGCAGCCATGGTAGC
                                                                                                                                                 5709 TAGTAAAATACCATATACAGAGATTACCCAAGGAAGCAFTGTCCFTTTAGGTGTCGTACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                             829 IGAACTCATTGCAACTGTCAAATATTTGTTTCATTTTGCTCTAATTGTAACATTTCTCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        242 ATTTTTGTTGGAGAATAATTTCGCACTTTCAAGACGTGGTGCCGTGTATTTCACATTAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5889 GTTTTTTGCAGATGGAAGTTTTTCAATCTCACGTCGCGGACTTCTTTACGTCACCCTGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          302 AAACTICGITITGGIATACCTATITAACGTAATTATTAAGCAGTTTAAGGATAGCTTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            362 ATTITICGACAATCTATCAAAAAAGACGATTCTAATTACAACGCTGAACGATGGGAAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         542 AGCTATAGAGTTTTCAACAAGGGAAGTGGTCGACCACGTCTTTATAAATCTACCAAGTGA
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                                                                                                                                                                                                                                                                                                                                                                                  182 AGAGTTTGAAAAACATTTAACTATAGTATAATATTTGCAATTTTTCTTACGGCAGTATC
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Gaps

Query Match 5.4%; Score 376.2; DB 3; Length 19966; Best Local Similarity 56.1%; Pred. No. 9.2e-42; Matches 780; Conservative 0; Mismatches 593; Indels 18;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New nucleic acid fragments containing exopolysaccharide operon, useful e.g. for increasing exopolysacchride synthesis in lactic acid bacteria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 fermented food product;
ATTGAAAAAGGATTAAAGTAGTAGTAATGAAGGATGGAGCAAAGTGATGGCTTTCACCATT
                                                                                                       AACAGTTGATGAGTATGAAAAATATACACCTGAACAAACGTCGTTTAAAGTTTTAAACC
                                                                                                                                                              AGGGATTACAGGTCTCTGGCAGGTTAGTGGTCGTAGTAATATCACAGACTTCGACGACGT
                                                                                                                                                                                                                                                                                                     TGTAAAACTAGACGTTGCTTATTTGGACGGATGGACAATCTGGCGTGATATCAAAATCTT
                                                                                                                                                                                                                                                                                                                                                ATTAAAGACAGTGAAAGTTGTAGTTGAGAGGAGGAAGTAAAGTAAAAGTATATGAAAGT
                                                                     TACAGTTGATGAATTTGAAAATATACTCCTGGTCAAAAGAGAGGATGAGTTTTAAAACC
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                                                                                                                                                                                                                                                       AGTICGGITGGACTIAGCATACATTGATAATTGGACTATCTGGTCAGATATTTTT
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(RHOD ) RHODIA CHIM.
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(DANO-) CIE DANONE SA
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Length 28170;

Query Match 5.4%; Score 376; DB 6; Length 281 Best Local Similarity 56.7%; Pred. No. 9.7e-42; Matches 782; Conservative 0; Mismatches 580; Indels

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                                                   <u>AAATTGGTATTATACAGTTGGTTGTGGTTGTTTTTTGCAGCCATGGTAGCTAGTAAATAC</u>
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  <u> AATTGGCATTATTTGATATGATAGCAGTTGCAATTTCTGCAATCTTAACAAGTCATATAC</u>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New nucleic acid fragments containing exopolysaccharide operon, useful e.g. for increasing exopolysacchride synthesis in lactic acid bacteria
                                                           AATTTGAAAAATATACTCCTGGTCAAAAGAGACGATTGAGTTTTAAAACCAGGGATTACAG
                                                                                                                        GTCTCTGGCAGGTTAGTGGTCGTAGTAATATCACAGACTTCGACGACGTGGTTCGGTTGG
                                                                                                                                                                                                                ACGITGCTTATTTGGACGGATGGACAATCTGGCGCGATATTAAAATCTTATTGAAAACAA
TTTATATATGTTTTAATTGGCGATATGAGTCTAGTTGGTACACGTCCACCTACAGTTGATG
                    GTCTTTGGCAAGTAAGCGGTCGAAGTGAATTACTGATTTTTGATGAAGTTGTAAAACTAG
                                                                                        AGTACGAATCTTATACACCGGAACAAAAACGTCGCCTCAGCTTTAAACCAGGTATTACTG
                                                                                                                                                                                                                                             TGAAAGTTGTATTGTTGAGAGGAAGTAAGTAAAAGTATATGAAAGTTTTGTTTGGTCG
                                                                                                                                                                                                                                                                          Sequence 15962 BP; 5026 A; 2706 C; 2993 G; 5217 T; 0 U; 20 Other;
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                                                                                                                                                                      Exopolysaccharide, lactic acid bacterium; eps; fermented food product;
TACAGTTGATGAATTTGAAAATATATACTCCTGGTCAAAAGAGACGATTGAGTTTTAAAACC
                      AGGGATTACAGGTCTCTGGCAGGTTAGTGGTCGTAGTAATATCACAGACTTCGACGACGT
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                                                                                                                                GTCTTTGGCAAGTAAGCGGTCGAAGTGAATTACTGATTTTTGATGAAGTTGTAAAACTAG
                                                                                                                                                                                                                                                                        Exopolysaccharide; lactic acid bacterium; eps; fermented food product;
                                                                   AGTACGAATCTTATACACCGGAACAAAAACGTCGCCTCAGCTTTAAAACCAGGTATTACTG
                                                                                                      GTCTCTGGCAGGTTAGTGGTCGTAGTAATATCACAGACTTCGACGACGTAGTTCGGTTGG
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Pred. No. 4.1e-41;
0; Mismatches 596; Indels
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(DANO-) CIE DANONE SA GERVAIS.
(RHOD ) RHODIA CHIM.
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Best Local Similarity 55.9%;
Matches 777; Conservative
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                     <u> AAGTCATATACCAAATGCTGATTTAAATCGTTCTGGAATTTTTTATCATAATGATGGTTCA</u>
                                                                                                                                                 AGAGITIGAAAAACAITIAACIAIAGIAIAAIATITIGCAAITITICITACGGCAGIAIC
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AACATTGGATGAGTACGAATCTTATACACCGGAACAAAAACGTCGCCTCAGCTTTAAACC
                                                  AGGGATTACAGGTCTCTGGCAGGTTAGTGGTCGTAGTAATATCACAGACTTCGACGACGT
                                                                       AGTTCGGTTGGACTTAGCATACATTGATAATTGGACTATCTGGTCAGATATTAAAATTTT
                                                                                                                                               TGTAAAACTAGACATTGCTTATATGGACGGATGGACAATCTGGCGTGATATCAAATATT
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0; Mismatches 596;
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55.9%; Pred. No. 4.1
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CIE DANONE SA GERVAIS.
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les 777; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New nucleic acid fragments containing exopolysaccharide operon, useful e.g. for increasing exopolysacchride synthesis in lactic acid bacteria
                                                                                                                                         product;
TACAGTTGATGAATTTGAAAATATACTCCTGGTCAAAAGAGAGGATTGAGTTTTAAACC
                   <u> aacatiggatgagtacgaatcttatacaccggaacaaaaacgtcgcctcagctttaaacc</u>
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                                                             <u>AGGTATTACTGGTCTTTGGCAAGTAAGCGGTCGAAGTGAAATTACTGATTTTGATGAAGT</u>
                                                                                  AGTTCGGTTGGACTTAGCATACATTGATAATTGGACTATCTGGTCAGATATTAAAATTTT
                                                                                                                            Sequence 25243 BP; 8278 A; 3819 C; 5072 G; 8074 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New nucleic acid fragments containing exopolysaccharide operon, useful e.g. for increasing exopolysacchride synthesis in lactic acid bacteria.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptococcus thermophilus eps11 operon #2.
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(RHOD ) RHODIA CHIM.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New nucleic acid fragments containing exopolysaccharide operon, useful e.g. for increasing exopolysacchride synthesis in lactic acid bacteria
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Best Local Similarity 55.5%;
Matches 766; Conservative
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                                                          4769 TTTTTTGCAGATGGAAGTTTTTCAATCTCACGTCGCGGACTTCTTTACGTCACCATGATT
                                                                                               AACTICGITITIGGIATACCIATITIAACGIAATIATIAAGCAGITITAAGGATAGCITITCIA
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                         TTTTTGTTGGAGAATAATTTCGCACTTTCAAGACGTGGTGCCGTGTATTTTCACATTAATA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TATTTTGCATTTTTTATATCTCGTATGCCAGTTGAATTTGAGTATAGAGGTAATCTGATA 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New nucleic acid fragments containing exopolysaccharide operon, useful e.g. for increasing exopolysacchride synthesis in lactic acid bacteria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 product;
GTCTCTGGCAGGTTAGTGGTCGTAGTAATATCACAGACTTCGACGACGTAGTTCGGTTGG
                                                                                   ACTTAGCATACATTGATAATTGGACTATCTGGTCAGATATTAAAATTTTAAAAGACAG
                                                                                                                                                       ACGTTGCTTATTTGGACGGATGGACAATCTGGCGCGATATTAAAAATCTTGAAAACAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4.9%; Score 346; DB 6; Length 12786; 57.2%; Pred. No. 1.1e-37; ive 0; Mismatches 529; Indels 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Exopolysaccharide; lactic acid bacterium; eps; fermented food
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                                                                                                                                                                                                                                                                                                                                           BP.
                                                                                                                                                                                                                                                                                                                                           ABA01433 standard; DNA; 12786
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Best Local Similarity 57.2
Matches 727; Conservative
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Search completed: April 29, 2005, 02:36:47 Job time : 3285 secs

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Perfect score:

Sequence:

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Run on:

Scoring table:

Searched:

Minimum DB Maximum DB

Database

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APPLICANT: Miyake, Katsuhide
APPLICANT: Watanabe, Masaki
APPLICANT: Watanabe, Masaki
APPLICANT: Jijima, Shinji
TITLE ON: INVENTION: Beta 1,3-galactosyltransferase and DNA encoding the same
PILE REPERENCE: 766.53
CURRENT PILLOTATION WUMBER: US/09/900,038A
CURRENT FILING DATE: 2001-09-21
PRIOR APPLICATION NUMBER: JP 2001-392
PRIOR PILLNG DATE: 2001-01-05
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO
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Pred. No. 3.7e-122;
0; Mismatches 917;
US-08-961-083-199
US-09-536-784-199
US-09-634-238-97
US-09-634-238-97
US-09-649-016-12776
US-09-949-016-12776
US-09-949-016-12940
US-09-816-028A-26
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US-09-949-016-12776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Streptococcus agalactiae type Ib
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                                                                                                                                                                                                                                                                                                                                                                                                US-09-900-038A-3; Sequence 3, Application US/09900038A; Sequence 3, Application US/09900038A; Patent No. 6828128; GENERAL INFORMATION:
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Sequence 1469, Ap
Sequence 14164, A
Sequence 1006, Ap
Sequence 893, App
Sequence 2107, Ap
Sequence 13, Appl
Sequence 13, Appl
Sequence 13, Appl
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Sequence 2987, Ap
Sequence 71, Appl
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.: /cgn2_6/ptodata/1/ina/PcTuS_COMB.seq:*
.: /cgn2_6/ptodata/1/ina/PcTuS_COMB.seq:*
                    version 5.1.6
- 2005 Compugen Ltd.
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US-09-134-000C-2987
US-09-134-000C-2344
US-09-107-532A-1469
US-09-949-016-14164
US-09-948-016-14164
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Gapop 10.0 , Gapext 1.0
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158.4 1152.6 1145.4 1145.4 1139.2 1139.2 1137.4 1127.4 1127.4 1127.2 1127.2 1127.2 1127.2 1127.2 1127.2 1127.3 1127.3

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Oy 1264 ITCGGTIGGACTTAGCATACATTGATAATTGACACTTGATAATTGACACTTGACTTGATGATGATGGTCTCAATATATCAATGAATG	Qy 1324 TAAAGACAGTGAAAGCTTGTATTGTTGAGAGGGGG 1749 TCCTAACGCTAAAGGTAGTTTTACTCGGGACAGG	1373	1427	1987	1547	1607 2049	Oy 1667 TGGAGGAAAGAGGATTTATATTGAGTATTTGAT 	Qy 1727 AAAACTAGITTATCCCGTAACAGATATTTTATT	Qy 1787 ATAICCTAAATCTATTAACTTGGGGAGTAITTTT DD 2229 TTAICCTAAGGCAATTAATTTAGGAGGAATTTTTTTTTTT	1847	1907	Qy 1967 TATAAAAATITCTCAGTTACAAAGAAATGGAAC 	2027	Qy 2087 TTGTTTCCTAGACAAAAAGTATGGTGAACATG	Qy 2147 AGAAGAATTTTACAAGATAATAATTTTATTTZ 	Qy 2207 AAAATTATTGAAGTTTCTAAGGAACTAACT 	Oy 2264 GAAAGAITAAAACAAAIAGTIGAAAAAAITTAATG	2324
193 AAACAITTAACIATAGIATAATAITTGGAATTTTTGTTAGGGAGTAICAITTTIGTTGG 252	TGGIATTGAAATACAGCTTTTACTATATTTTCATATGAGTTCATTATTTTTTTT	6/8 AAAACICITITIACAACGACATICCITITITACITITIATIGCIAIGAATICGATT 737 313 IGGIATACCIAITTAACGIAATTAITAAGCAGITIAAGGATAGCITCTATITICGACAA 372 	373 TCTATCAAAAAAGACGATTCTAATTACAACGGCTGAACGATGGGAAAATATGCAAGTTT 432 	433 TATTTGAATCACATAAACAAATTCAAAAAATCTTGCATTGGTAGTTTTTAGGTACAG 492 	493 AAATAGATAAAATTAATCATTACCGCTCTATTATTCTGTGGAAGAGCTATAGAGT 552 	553 TTTCAACAAGGGAAGTGGTCGACCACGTCTTTATAAATCTACCAAGTGAGTTTTTAGACG 612 	613 TAAAGCAATTCGTTTCAGATTTTGAGTTGTTAGGTATTGATGTTAACGTTG 663 	ACTECGTTGAAAAAAAAAAACCAACTGCTAGGTGACC		784 TITIGGATATACTCGGAGCGGTAGTCGGGTTAATTATTGTGGTATAGTTTCTATTTGT 843 	844 TAGTICCAATTATICGTAGAGAIGGIGGACCGGCTATTITIGCTCAGAAACGAGTIGGAC 903 	904 AGAATGGACGCATATTTACATTCTACAAGTTTCGATGTATGT		1024 AAACGATCCTAGAATTACTCCAATTGGACATTTCATACGCAAAAACAAGTTTAGACGAGT 1083 		TATACTCCTGGTCAAAGAGAGGATTGAGTTTTAAACCAG		1629 GAATCACTGGTTTGTGGCAAATACTGGTAGAATAATAATTACTGATTTTGATGAAATCG 1688
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
SEQUENCES RELATING TO STREPTOCOCCUS
THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
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COMPUTER: «Unknown»
OPERATING SYSTEM: «Unknown»
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CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
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58.3%; Pred. No. 5.5e-66;
ive 0; Mismatches 552;
                                                                                                                                                                                                                FILE REFERENCE: PATHOL-07A
CURRENT APPLICATION NUMBER: US/09/583,110
CURRENT FILING DATE: 2000-05-26
FRIOR APPLICATION NUMBER: US 60/085,131
PRIOR FILING DATE: 1998-06-30
PRIOR FILING DATE: 1998-05-12
PRIOR APPLICATION NUMBER: US 60/085,131
PRIOR FILING DATE: 1998-05-12
PRIOR FILING DATE: 1998-05-12
PRIOR FILING DATE: 1997-07-02
NUMBER OF SEQ ID NOS: 5322
SERVING FILING DATE: 1368
                                                                                                        Sequence 1332, Application US/09583110 Patent No. 6699703
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2769 AATTGAA 2775
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Matches 789;
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                                                                              614 AAAGCAATTCGTTTCAGATTTTGAGTTGTTAGGTATTGATGTAAGCGTTGATATTC
                                                                                                             696 TGGAGAGCTTGTCTCTCAGTTGAACGATGGGAGTTGATGTAACAGTCAATCTAAATGC
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                                                                                                                                                                                                                                                                                                                                                                                                                        TATTCGTAGAGATGGTGGACCGGCTATTTTTGCTCAGAAACGAGTTGGACAGAATGGACG
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                                                                                                                                                                 674 ATTCGGTTTTACTGCGTTGAAAACAAAAAATCCAACTGCTAGGTGACCATAGCATTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue CITY: Rockville STATE: MD COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              254 GAATAATTTCGCACTTTCAAGACGTGGTGCCGTGTATTTCACATTAATAAACTTCGTTTT 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               342 AGATCGATTTAGTATTTCCAGAAGAGCATGATTTACTTCCTCCTATTACATGTTCTCTT 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGTATACCTATTTAACGTAATTATTAAGCAGTTTAAGGATAGCTTTCTATTTTCGACAAT 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTATCAAAAAAGACGATTCTAATTACAACGGCTGAACGATGGGAAAATATGCAAGTTTT 433
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AATAGATAAAATTAATTTATCATTACCGCTCTATTATTCTGTGGAAGAAGCTATAGAGTT 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         102 ATTGGCCATAGTCCAGAGTTTTCTTGTTATTTTATTGGCTTATCTACTTAGCACTGTGAG 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGAAACAGAGATTGTTTCAACAACAGCTATTGTACTTTATATCCTCCACTATTTTGCCTT 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGTCTATGTGCTAAACCGATTTATCAAGTGGTATTGGAAGCGGGCTTATCCCAACTTTAA 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGGAAGTAAGAAGATTCTCCTACTTACAGCAACTTCTCGTGTCGAAAAGGTATTGGATAG 521
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Best Local Similarity 58.3%; Pred. No. 5.5e-66;
Matches 789; Conservative 0; Mismatches 552;
        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,433
FILING DATE: 30-0un-1998
PRIOR APPLICATION NUMBER: 60/085131
APPLICATION NUMBER: 60/08131
FILING DATE: May 12, 1998
APPLICATION NUMBER: 60/05153
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Denek
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature;
LOCATION: (B) LÖCATION 1...1443
SEQUENCE DESCRIPTION: SEQ ID NO: 2303:
US-09-107-433-2303
                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 2303:
SEQUENCE CHARACTERISTICS:
LENGTH: 1443 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: Circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: double
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924401 AATCTGGCTAAACTATCTTCTCGTATTTTGAAACGAACCATGGATATTGTTGTTGGTTCC 924460
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                                                     924997 GGTTTTAAATCGTGATGGAGCTTATTAACGTTATTT 925032
1340 TGTATTGTTGAGAGAGGAAGTAAGTAAAGTATAT 1375
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Pred. No. 6.7e-19;
); Mismatches 266;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/09/643,990A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: 3 1/2 inch diskette
COMPUTER: Dell Pentium
OPERATING SYSTEM: MS DOS V6.22
SOFTWARE: ASCII Text
                                                                                                                                                                                                                                                                                                                                          Hamilton O. Smith
J. Craig Venter
TITLE OF INVENTION: The Nucleotide s
the Haemophilus
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APPLICATION NUMBER: 08/426,787
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Scien
STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                 APPLICANT: Robert D. Fleischmann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Kenley K. Hoover
REGISTRATION NUMBER: 40,302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 1830121 base pairs
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CLASSIFICATION: <Unknown>
                                                                                                                                                                             Sequence 1, Application US/09643990A Patent No. 6528289 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 1995-04-21
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STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                        Mark D. Adams
Owen White
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
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Best Local Similarity 56.4
Matches 359; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Rockville,
STATE: MD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF
                                                                                                                                                          US-09-643-990A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   924521 GGTGGTAATGCTATTTATGGGCATCCTAGAATTGGTCGTAATGGAAAAACATTTAACTGT 924580
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     924641 GATCCTGAAGCAAGAGCTGAATGGGAAAAAGATTTTAAATTAAAGAATGATCCTAGAATT 924700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          924760 TGTTTTAAAAGGTGAAATGAGTTTAGTTTGGGCCTCGCCCAATTGTAATTGATGAGGTAGA 924819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  124820 GCGTTÄTGAAGAAACGTÄGÄTTATTACTTAATGGCAAGACCCGGTÄTGACAGGCTTTG 924879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1039
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1280 ATACATTGATAATTGGACTATCTGGTCAGATATTAAAATTTTTATTAAAGACAGTGAAAGT 1339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         747 AATTTTTATAAGCCTAGTCATATCATGAAACGACTTTTGGATATACTCGGAGCGGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGTGGACCGGCTATTTTTGCTCAGAAACGAGTTGGACAGAATGGACGCATATTTACATTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   983 ---CCAAAACCAGATGCAAGGGTGGGTATGTTTTAAAATGGGAAAAACGATCCTAGAATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1040 ACTCCAATTGGACATTTCATACGCAAAACAAGTTTAGACGAGTTACCACAGTTTTATAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1100 TGTTTTAATTGGCGATATGAGTCTAGTTGGTACACGTCCACCTACAGTTGATGAATTTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          324880 GCAAGTCAGCGGACGTAATAATATC---GATTATAATACTCGCGTTTATTTTGATTCTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    807 GTCGGGTTAATTATTTGTGGTATAGTTTCTATTTTGTTAGTTCCAATTATTCGTAGAGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1830121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches 266; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 158.4; DB 4
Pred. No. 6.7e-19;
                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/557,884
FILING DATE: 25-Apr-2000
FLASSIFICATION: <UNKNOWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/476,102
FILING DATE: UNN 5-1995
                                          MEDIUM TYPE: 3 1/2 inch diskette
COMPTTER: Dell Pentium
OPERATING SYSTEM: MS DOS V6.22
SOFTWARE: ASCII Text
                                                                                                                                                                                                                                                                                                                                                                   NAME: Michelle S. Marks
REGISTRATION NUMBER: 41,971
REFERENCE/DOCKET NUMBER: PB186P3
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 1830121 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FELEPHONE: 301-309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 301-309-8439
                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 56.4
Matches 359; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR
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1851 ATTCTCTATAAATAATATTGATTTAGTCACAAGATTGGAGAATTACCCCTTTAAGTTAAA 4910
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GIGCAAGCITIATICACGAGATATIATAAAAGATATAAAATICCAAATIAATAATAGAAG 4730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 192 AGTACGIGIGAICCÁTAAAGAAAACGGCGGATTAAGCAGTGCTAGAAHGCGGGGATTGA 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               603 TGTTTCCAATGAAGAGAAATATTTCTATCTTCAAAGAAATGATAGTATTATGGGAAAAAG 662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       132 TGATGGATCTCCTGACAATAGCGGGAAAATCTGTGATGAGTATGCTGAAAAAGATAATCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1431 ACATGCAACAGGTAAATATATTGCTTTTGTCGATTCTGATGACTATATAGAAGTTGCAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AACGAGAGAGAGACTGTAAAAGAATTTTTGTCAGGATCTAATATAGAAAATAATGTTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGATGGAAGTACTGATTCTGAGAAAATTTGCTTAAAACTATATGAAGAACGATGGAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              252 TGTTGCGAGAGGCAAATACTTAGGCTTTGTTGACAGTGATGATTATTATTGATGATGATAT
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                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                          Length 984;
                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                     Score 152.6; DB 4;
Pred. No. 1.6e-18;
0; Mismatches 354;
                                                                                                                                                    NAME/KEY: misc_feature;
; LOCATION: (B) LOCATION 1...984;
; SEQUENCE DESCRIPTION: SEQ ID NO: 2527:
US-09-107-532A-2527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAGAGAGTTTAGTCATTATTTTGATGC 4937
                                                                                                                         ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 2987, Application US/09134000C
; Patent No. 6617156
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         TOPOLOGY: circular MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                     Query Match 2.2%;
Best Local Similarity 51.4%;
Matches 384; Conservative
                                                   HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-134-000C-2987
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
924820 GCGTTATGAAGAAAACGTAGATTATTACTTAATGGCAAGACCCGGTATGACAGGGCTTTG 924879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  324880 GCAAGTCAGCGGACGTAATAATATTC---GATTATAATACTCGCGTTTATTTTTGATTCTTG 924936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---CCAAAACCAGATGCAAGGGTGGGTATGTTTTAAAATGGGAAAAACGATCCTAGAATT 1039
                                                                                                                                                                                                                                                                                                                                                         1160 AAAATATACTCCTGGTCAAAAGAGACGATTGAGTTTTAAACCAGGGATTACAGGTCTCTG 1219
                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCAGGITAGTGGTCGTAGTAATATCACAGACTTCGACGACGTAGTTCGGTTGGACTTAGC 1279
                                                                                                                       324641 GATCCTGAAGCAAGACTGAATGGGAAAAAGATTTTAAATTAAAGAATGATCCTAGAATT
                                                                                                                                                                                                                                                                  TGTTTTAATTGGCGATATGAGTCTAGTTGGTACACGTCCACCTACAGTTGAATTTGA
                                                                                                                                                                     1040 ACTCCAATTGGACATTTCATACGCAAAAACAAGTTTAGACGAGTTACCACAGTTTTATAA
                                                                                                                                                                                                                                                                                                           924760 TGTTTTAAAAGGTGAAATGAGTTTAGTTGGGCCTCGCCCAATTGTAATTGATGAGCTAGA
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ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1340 TGTATTGTTGAGAGGGGAAGTAAGTAAAGTATAT 1375
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PRIOR APPLICATION DATA: APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: GTC-012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Application US/09107532A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 2527:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 984 base pairs
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STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 02354
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: ASCII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Waltham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2527, Applicat
Patent No. 6583275
GENERAL INFORMATION:
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                     APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE EOF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 032796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1997-08-13
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR FILING DATE: 1997-08-15
SOFTWARE: PATENTIN VETSION 3.1
SEQ ID NO 2987
LENGTH: 993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             486 TGTAAATAAGTTATATAAACGAAAACTCTTTGCGGATTTAAGATATCCTAAAGGAAAGTA 545
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 993;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
2.1%; Score 145.4; DB 4; Length
Best Local Similarity 52.0%; Pred. No. 3.2e-17;
Matches 382; Conservative 0; Mismatches 341; Indels
                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Enterococcus faecalis
US-09-134-000C-2987
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GENERAL INFORMATION:
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Sequence 71, Application US/08961527
Patent No. 6420135
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INFORMICS: 31
NUMBER OF SEQUENCES: 391
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6452
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6333 ATTTTCAGAAATGGATCACCGAATTCTCTATATAGAACAAGAAAATGCTGGTCTTTCTGC 6392
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 32768;
                                                                                                                                                                                                                                                  ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2.1%; Score 144.6; DB 3;
52.3%; Pred. No. 9.1e-17;
tive 0; Mismatches 329;
                                                                                                                                            ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                              US/08/961,527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB34
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
INFORMATION FOR SEQ ID NO: 71:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36,373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32768 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 2.1'
Best Local Similarity 52.3
Matches 368; Conservative
                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM:
SOFTWARE: ASCII TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                         STATE: Maryland
                                                                                                                                                                                                                                 USA
                                                                                                                                                                                                                                                20850
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US-08-961-527-71
                                                                                                                                                                                                                               COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        211 GCATTTCGATGGCACGAGGACGGTATTTGCAATTTCTGGATGCAGATGATCATTTTGAAG 1270
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                                                               618 GAAGAGACTGTAAAAGAATTTTTGTCAGGATCTAATATAGAAAATAATGTTTGGTGCAAG 4677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1918 TTTAGTCATTATTTTGATGCAAAGTTATTAAAGAGAAGGTTAAATGTTTAAACAAAATG 4977
TTTCTTCTGAAGAAGAGTTGAGCGAGATATATATGGCAATATCCCGATAAATACAAT 444
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                                                                                                         445 CAATTGATTGACTTAAAA---ACGACGGATTTAATTGTACAAGTTTATCCATGGAATGCC
                                                                                                                                                   CTTTATTCACGAGATATTATAAAAGATATAAAATTCCAAATTAAATAGAAGTATTGGT
                                                                                                                                                                                           ATTTATAAAAAAGTATGAGAAAGAAACGTAACTTGGGATGAGGAAATTAAAAGT
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTEROCCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR PILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: Patentin version 3.1
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Sequence 2344, Application US/09134000C
Patent No. 6617156
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Sequence 14164, Application US/09949016

Bacent No. 6812339

Bacent No. 6812339

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLO01307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-414

PRIOR FILING DATE: 2000-10-20
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                                                                                                                                                                                                                                                                    APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
  1451 ATGATAAATTATTTTTTTTAGAATACATCAAAGAAAATAACTTGGTAAACTTAGAACAAT 1510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5212
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                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 MAY 1998
APPLICATION NUMBER: 60/051571
FILING DATE: JULY 2, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc feature
LOCATION: (B) LŌCATION 1...1002
SEQUENCE DESCRIPTION: SEQ ID NO: 1469:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Enterococcus faecium
                                                                                                                                                                                                       Sequence 1469, Application US/09107532A Patent No. 6583275 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 1002 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: circular
MOLECTLE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 1469:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                       7310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: Massachusetts
                                              TTTTCAAGAGAAT 5711
                                                                                            TTGTTGGCGAGGAT 1524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 02354
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: ASCI.
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                                                                                                                                                            RESULT 10
US-09-107-532A-1469
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APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PREUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709-2004001
CURRENT APPLICATION NUMBER: US/09/489, 039A
CURRENT FILING DATE: 2000-01-27
PRIOR FILING DATE: 1999-01-29
PRIOR FILING DATE: 1999-01-29
    17492 AAATATATATTATATATTAATTATATATATTGATAATTATGTTATGAGATATATGTATATA 17433
                                                                                                                                              .7312 TATĀTTAAATAATATTTTTTATĀTĞTTĀTĀTĀTACATTATTĀGĀTATTCTĀTĀTTA 17253
                                                                                                                                                                                                                                                                                                                                                                                                ATARAGIATTAGAAAACAATATTTAAT-TTGGATATGGAATATCCGAATATTCAGTTACG 3926
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                                                   3748 TATTTGTAATACTACTTATTATTATAATACTGAATTGCTTTACCATGAAATTTTGGCTG
                                                                                                                 TITATAATICTAGAGAATCAAGTAACGAAGCTAGATTTATTATTATCAAGGAAGTATTG
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                                                                                                                                                                                                                                        3927 GGAACTTGGCTCGGAAGTCATTCAGGCTATATATCATTTTTTTATAAATCAGGAATAGTT
                                                                                                                                                                                                                                                                                                    3987 GGGTTGATTTTACTGATGTTTTTTTTTTTTATAAAAAAAGTTATGGAGTTAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 1.9%; Score 132.2; DB 4; Best Local Similarity 54.1%; Pred. No. 8.5e-15; Matches 340; Conservative 0; Mismatches 278;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 1006, Application US/09489039A; Patent No. 6610836; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                               GATCCGATTATTATAT 4125
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                                                                                                                                                                                                                          16;
                                                                                                                                                                                             Length 18773;
                                                                                                                                                                                         Score 132.6; DB 4; Length
Pred. No. 1.2e-14;
0; Mismatches 659; Indels
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-031,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 14164
                                                                                                                                                                                         Query Match 1.9%;
Best Local Similarity 47.2%;
Matches 604; Conservative
                                                                                                                            TYPE: DNA
ORGANISM: Human
                                                                                                                                                           US-09-949-016-14164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17994 ATATAATATATATATATATATATATATATATATATACATTACATATATATATATATATATAT 18053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2330 ATATTTGATAATGGCTTATCATAATTTTTCTCAGATTTTTACTGGAGAGGGATACAGATAT
                                                                                                          AATAGGATATATGAACGAGTTAAATGTTACAGATTATTTCCTAATATATCAGAAAAAACT
                                                                                                                                                                                                                                                                                                                                                                                                         ATTGGGTTTCGCTTCCACATGATTTTTGTGGCAATTCTTTTATCAAATGAAAACGAAACAG
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                                  2390 TATCATCTTCTCTCAGGAGAATGCACCATTAGTTCCTTCAGAATACCTGTATAATTAT
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Fatent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REPRENCE: CLOOU307
CURRENT APPLICATION NUMBER: 00/9/949,016
CURRENT PILING DATE: 2000-04-14
FRIOR APPLICATION NUMBER: 60/241,755
FRIOR APPLICATION NUMBER: 60/241,755
FRIOR FILING DATE: 2000-10-03
FRIOR FILING DATE: 2000-10-03
FRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FREESEQ for Windows Version 4.0
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                                                                                                                                                              1256 Argricciraaaggggagargagririagragggccacgccarcarracagcggarraag 1315
                                                                                                                                                                                                    AAAAATATACTCCTGGTCAAAAGAGACGATTGAGTTTTAAACCAGGGATTACAGGTCTCT 1218
                                                                                                                                                                                                                                                                                                               GGCAGGTGAGCGGGCGTAGTGTC---GATTATGATACTCGTGTGTACTTGGATGCGT 1432
                                                                                                                                                                                                                                                                                                                                                     CATACATTGATAATTGGACTATCTGGTCAGATATTAAAATTTTTATTAAAGACAGTGAAAG 1338
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TACTCCAATTGGACATTTCATACGCAAAAACAAGTTTAGACGAGTTACCACAGTTTTATA
                                                                                AGCGATATAACGATGAGGTCGACTACTATTAAGTAAACCTGGGATGACTGGGCTAT
                                                                                                                                                                                                                                                                             GGCAGGTTAGTGGTCGTAGTAATATCACAGACTTCGACGACGTAGTTCGGTTGGACTTAG
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                                                                                                                                                                                                                                                                                                                                                                                                                            TTGTATTGTTGAGAGAGGGAAGTAAGTAA 1367
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Best Local Similarity 45.3%;
Matches 595; Conservative C
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US-09-949-016-14164
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US-09-949-016-14164
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6293 TAATTCGGAAGAAATTTGTTTAGCATATGCGAAGAAAGATAGTCGCATTCGTTATTTAA 6352
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                     Sequence 2107, Application US/09107433
Patent No. 6800744
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE
THERAPEUTICS
NUMBER OF SEQUENCES: 5206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24 AATTAGTGTGATTGTGCCAGTCTATAATGTGCCCCAGTACCTAGAAAATCGATAGCTTC
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                                                                                                                                                                                                                                       GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 127.4; DB 4;
Pred. No. 5.8e-14;
0; Mismatches 306;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,433
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...996
SEQUENCE DESCRIPTION: SEQ ID NO: 2107:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Ariniello, Famela Deneke
REGISTRATION VUMBER: 40,489
REFERENCE DOCKET NUMBER: GTC-011
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 60/ 085131
FILING DATE: May 12, 1998
APPLICATION NUMBER: 60/051553
                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: <Unknown>
OPERATING SYSTEM: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                        STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (781)893-5007
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 996 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 2107:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                        STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: <Unknown>
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Best Local Similarity 51.2%;
Matches 327; Conservative
                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME
                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                  CITY: Waltham
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    JS-09-107-433-2107
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                                                            GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al.

APPLICANT: Lynn Doucette-Stamm et al.

TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus

TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus

TITLE OF INVENTION: NUCLEIC Acid and Amino Acid Sequences Relating to Streptococcus

TITLE OF INVENTION: NUCLEIC Acid and Amino Acid Sequences Relating to Streptococcus

TITLE OF INVENTION: NUMBER: US/09/583,110

CURRENT FILING DATE: 1998-06-30

PRIOR PILING DATE: 1998-06-30

PRIOR PILING DATE: 1998-05-12

PRIOR PILING DATE: 1998-05-12

PRIOR PILING DATE: 1997-07-02

NUMBER OF SEQ ID NOS: 53.22

SEQ ID NOS: 53.22
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Pred. No. 5.7e-14;
0; Mismatches 306;
                   Sequence 893, Application US/09583110
Patent No. 6699703
                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: DNA
; ORGANISM: Streptococcus pneumoniae
US-09-583-110-893
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Matches 327; Conserv
-09-583-110-893
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MOLECULE TYPE:
 ; MOLECULE TYPE:
; HYPOTHETICAL:
; ANTI-SENSE: NC
US-08-487-826B-13
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APPLICANT: Chitnis, Chetan
APPLICANT: Chitnis, Chetan
APPLICANT: Miler, Louis H.
APPLICANT: Peterson, David S.
APPLICANT: Su, Xin-zhaun
APPLICANT: Wellems, Thomas B.
APPLICANT: Wellems, Thomas B.
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
                 6472
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                                              264 TTATCTGATTTTTÄTTGACTCÄGÄTGÄTTATÄTCCÄTCCAGÄAATGÄTTCÄGAGCTTÄTÄ
              CTACTTAGCTTTTATAGACTCAGATGATTTTATTCATTCGGAGTTCATCCAAGGTTTACA
                                                                                CGAAGCAATTGAGAGAGAGAATGCCCTTGTGGCAGTTGCTGGTTATGATAGGGTAGATGC
                                                                                                                324 TGAGCAATTAGTTCAAGAAGATGC-----GGATGTTTCGAGCTGTGTGTCATGAATGT
                                                                                                                                                TTCGGGGCATTTCTTAACAGCAGAGCCGCTTCCTACAAATCAGGCTGTTCTGAGCGGCAG
                                                                                                                                                                                                                   GAATGTTTGTAAAAAGCTGCTAGAGGCGGATGGTCATCGCTTTGTGGTGGCCTGTAATAA
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                                                                                                                                                                                                                                                                                       6653 ACTCTATAAAAAGAACTATTTGAAGATTTTCGATTTGAAAAGGGTAAGATTCATGAAGA
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ZIP: 92660
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,826B
FILING DATE: 10-SEP-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Israelsen, Ned
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: NIH121.001CP1
TELECOMMUNICATION NOCREASED
                                                                                                                                                                                                                                                                                                                                                                                                                              CTTGTACTATTATGTTGACCGAGAAAATAGTATCACAAC 6811
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STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: California
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; Patent No. 5993827
; GENERAL INFORMATION:
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TELEPAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 13: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 19124 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 4:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe Ma:
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US-08-487-826B-13/c
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                                                                                                                                                                                                                                                2960 TAAAAATAGAAAATAAATCTAAATTTAAAGAAATTATTACTAAAAAATAAAATAGTTGAT
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                                                                                                                        2900 ATGATTCTATTGATGAATTGCTAAATGCAAGAAATTTAGGTTTTTTATTTGCTAGAAAGT
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                                                                  Gaps
                                                               49;
      Length 19124;
                                                            Indels
   Score 125.8; DB 2;
Pred. No. 2e-13;
); Mismatches 1877;
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   1.8%;
Query Match
Best Local Similarity 42.5
Matches 1421; Conservative
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aagtattgataaagtattagaaaacaatattttatttggatatggaatatccgaatattc 3919 	AGTTACGGGAACTTGGCTCGGAAGTCATTCGGGCTATATATA	AATAGTTGGGTTGATTTTACTGATGTTTTTTTTTTTTTT	AGTIPAIGGGGAACGGCACTAITITAITITACAICAITAGCCAIATITITICAIAIAGA 4099 	AACAATAGATCCGATTATTATTATATTAGTACTATTCTTTCAATAGGTATTTGGAA 4159 	TAATATAAATTTIAAAAAGGATATGGACAAAAAATGAATGATTTAATTTCAGT 4214 	TATTGTACCAATTTATAATGTCCAAGATTATCTTGATAAATGTATTAACAGTATTATTAA 4274 	CCAAACATATACTAATTTAGAGGTTATTCTCGTAAATGATGGAAGTACTGATGATTCTGA 4334	GAAAATTIGCTIAAACTAIAIGAAGAAGGATGGAAGAATTAAATATTACAAGAAAT 4391 	TAATGGCGGTCTAGCAGATGCTCGAAATTTCGGACTAGAACATGCAACAGGTAAATATAT 4451 	TGCTTTTGTCGATTCTGATGACTATATAGAAGTTGCAATGTTCGAGAGAATGCATGATAA 4511	TATAACTGAGTATAATAGCGGTATAGGAGGATAGATTTTTGTTTAGTAGACGAAAACGG 4571	GTATACAAAGAAAAAAAAAAATAGTATTTCATGTCTTAACGAGAAGAAGAGTCTGTAAA 4631 	AGAATTTTTGTCAGGATCTAATATGAAAATAATGTTTGGTGCAAGCTTTATTCACGAGA 4691	TATTATAAAAGATATAAAATTCCAAATTAATAGAAGTATTGGTGAGGATTTGCTT 4749	TITAAITITGGAGGICTIGAACAATGTAACACGTGTAGTAGTAGTACTAGAGAATATTAT 4809 	TATAATTATGTCATTCGTAACAGTTCGCTTATTAATCAGAAATTCTCTGTAAATAATATT 4869	GATTTAGTCACAAGATTGGAGAATTACCCCTTTAAGTTAAAAGAGAGTTTTAGTCATTAT 4929	TTTGATGCAAAAGTTATTAAAGAGAAGAGTTAAATGTTTAAACAAAATGTATTCAACAGAT 4989
3860 AAGTATTGA 	3920 AGTTACGGC 6184 CTTTAAAGT	3980 AATAGTTGC 6124 ATATATATA	4040 AGTTAATGC 6064 AGAATAAAT	4100 AACAATAGA 	4160 TAATATAA 	4215 TATTGTACC	4275 CCAAACATA 5824 GTACAAAA	4335 GAAAATTTC 5764 AGACATATP	4392 TAATGGCGC	4452 TGCTTTTG1 	4512 TATAACTGA S584 TTAACTAAT	4572 GTATACAAA 5524 ATATAATA	4632 AGAATTTT7 5464 TCCTTAATA	4692 TATTATAAA 5404 CATTTTAA	4750 TTTAATTTC 5344 TTTCCTTA1	4810 TATAATTA1 5284 TATATATG	4870 GATTTAGTC	4930 TTTGATGC

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5649 5709 4392 5769 5829 5889 5949 6009 5049 5289 5349 5469 5589 4512 4223 TITTAAITITITAGAAAICITITATAAAAAAITAITAACITTAACITGITAAAAGIAICIAACA 6069 5107 4991 4931 5229 4871 4811 4751 5409 4691 4632 5529 4572 4452 4283 4391 TTAAATTAATAAAAAAATTTATTGTGACATTT---ATGCTTAATTTTTTAAATATTA 4335 1222 CTTTAACAACTATCCTTTTACACATTCTTATGTTATTTTATAATAAAAAGGAACCAGTTGT 4163 5164 TAATTAGTCCATAATATTCATCAAAAAAAACACAAAATCGAAATTTCATTATGTAAATG--5050 TITAAGATAAAATAATATATATATATTTTATCCTATTACAGTAACATTTTTA 4930 AAATTTTCATAAATATTATGAATTTTCCCCTTTATAATAACTAATAATATATAACATAAA 5950 AAGTATTTTATTATAGCTTAATGTTTAAATAGGAAAACAGTCTATTTTTGACAAAT TGTTTGGATAATGAGTTCTTGCCAATATTAGAGTCTTATCGAAAAGAAATACGTAGATAT 5050 CCATTTATTAAAGCGAAAAGATATTTATCAAGAAAGCATTTAGTTACGTTGTATTTGATG 5110 AAATTTTCGCCTAAACTATATGTAATGTTATATAAGAAATTTCAAAAGCAGTAGAGGTAA AAATGGATAAAATTAGTGTTATTCCAGTTTATAATGTAGATAAATATTTAAGTAGTT GTATAGAAAGCATTATTAATCAAAATTATAAAATATAGAAATATTATTGATAGATGATG 4870 AATATATTTCTTCTATTTATTACTATATATAATGTTCTGTGTTACTTATTAATATA 4810 TACAATAATATAAATATACCATATTTTATATTCATTGACACTATGACTACATATGAATAT AAATTTTTTCACTAATCATAGTGGAGTATCAAATGCTAGAAATCATGGAATAAAGCGGA 1750 ATTATTAGAATACCATACATACTAAAAAACAATTATATTAATATATATACGATACATA 5410 GTACAGCTGAATATATTATGTTTGTTGACTCTGATGATGTTGTTGATAGTAGATTAGTAG 4690 -AACAATATTACATAATCTCTAAATTATGAATGCAACATGTTTGTATAAGTTACAACTAT 4631 TTCACCAATTATACTATATATTATTATATGCATATTTCCATTTTAAAAGTTTTT 5530 CITITICAGAAAATATAAATTATTTGAAGTGAATAATCCAAATATTGAAGCAA 4571 TTTTTGTCATCATATTTATATATACTCCATGCATATTTCATATTATAATAAGTAA 5590 TTAATACCGTGCAGGACATGGGAGAAAAATTTTATGAATTTTGTATATAATAATATTT TITCTACTCCTGTTTGTAAACTATATAAGAAAAGATAACATAACAGATCTTTTTCAAGAGA 5710 ATCAATGGTTAGGAGAGATTTACTTTTAATCTGCATTATTAAAGAATATAGAG TTAGTTATTTGACTGAACATCTTTATTTTTATAGGAGGGTATACTAAGTACAGTAAATT 4334 TTTATAATATTTCTTATTATATATATTTTTTTA-----ATTACAATTATGCAAAGTT 5830 CITITAAAGAAGGIGIGITITITGCAATITGGAAAATTIGCAAAAACAAGIGAIAGTAITGI TTAAGCAAATATATGGTGAGGATTTTTGACGTATCAATTGTTAAAGATACTATACGTTGGC racrararigraaraggricerraagargaaracararararargrigarrar----aar ----Tagriaarirariaaaargggacaarriririraaargriaaraggaaccri 1990 TGCTTTCCATTTTTTCTTCTTGTTTTTTTTTTTTTTAACTTATAACTATATCATATACAA 5770 4990 5106 5170 5230 5350 5650 5890 6010

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TTATTCTATCGTATAAAATTTAAAATTTATAAATTAAAACAAATTAGAAAAAATTTAG 4048
                                                         TATTATGGTTATAATAGGAAGATATCATGGATACTATTAGTAAAATTTCTATAATTGTAC 6189
                                                                             3987 ATATATATTTGTATAATGGAAAGCTAATGGTGCCATATTAAAAAATTATAATAACAACTT 3928
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                                  ATATTTTATTATTATACTTTTTATATACAATAAATATTCAGATTCTAATGAGGAA
                    AAAATTCTTTGTCTAAAAATTTTTGTATAAGAATTGTTTCGAACAAAGTTTTTAAAAAA
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                                                                                                                                                                 1.8%; Score 125.8; DB 4; Length 95255;
Similarity 45.6%; Pred. No. 2.8e-13;
03; Conservative 0; Mismatches 1047; Indels 29;
                                                                                                 CTA-TATATATGTAGAAAATATTTATCTAAATGTATAGATAGCAT 6235
                                                                                                                    3927 ATATTAAACAATTTTTATAATAAAAAAAAAAAAAAAAT 3881
                                                                                                                                                                                                                                                                                                                                                                                                       ; LOCATION: (1) ... (95255)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17067
                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc feature
LOCATION: (1)...(95255)
                                                                                                                                                  RESULT 17
US-09-949-016-17067/c
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Best Local Simil
Matches 903; C
4107
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; Sequence 1, Application US/08597236; Patent No. 5733765; GENERAL INFORMATION:
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IBM PC compatible
double
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                  linear
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: U.S.A.
                                                                           Local Similarity
les 325; Conserv
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STRANDEDNESS:
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              ; TOPOLOGY:
US-08-961-527-86
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TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
NUMBER OF SEQUENCES: 391
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
                                                           12261 AATATATTATATATATATA-TAATATATATTATATAAATATATATATATATATAAATAA 42203
                                                                                                                                                                                                                                                                                                                                                                              12082 TITGIATATAGAATTATAATTCTATGITATATTTTGTATATGATATAGAATTATA 42023
                                                                                                                                                                                                                                                                                  3958 TAICATITITIATAAATCAGGAATAGTTGGGTTGATTTTACTGATGTTTTCTTTTTTT 4017
                             AATTTGCTTGGATAAAAAGCTAATAGTAATATTTGTAATACTACTTATTATTTTAAATA 3777
                                                                                          CTGAATTGCTTTACCATGAAATTTTGGCTGTTTATAATTCTAGAGAATCAAGTAACGAAG 3837
                                                                                                                                                       3898 GATATGGAATATCCGAATATTCAGTTACGGGAACTTGGCTCGGAAGTCATTCAGGCTATA 3957
                                                                                                                                                                                                                                                                                                                                               4018 ATGTTATAAAAAAAGTTATGGAGTTAATGGGGAAACAGCACTATTTTTTACATCAT 4077
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                                                                                                                                                                                                                                                                                                               ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP VECTE 486/33
OPERATING SYSTEM: MSDOS VERSION 6.2
SOFTWARE: ASCII Text
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 86, Application US/08961527 Patent No. 6420135 GENERAL INFORMATION:
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CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: P834
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 86:
SEQUENCE CHARACTERISTICS:
LENGTH: 19300 base pairs
TYPE: nucleic acid
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6533 TTCGGGGCATTTCTTAACAGCAGAGCCGCTTCCTACAAATCAGGCTGTTCTGAGCGGCAG 6592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTATGCTAATGATGAAGCCCACAGTCAGCCAATCAGGATGACTATTTTGTCTGTGATTC 4163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1162 TCAAACATTTCTAAAGGAATACCTCATAGGTGAAAAAATACCTGGGACGATTTGCAATAA 4103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6653 ACTCTATAAAAAAGAACTATTTGAAGATTTTCGATTTGAAAGGGTAAGATTCATGAAGA 6712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4102 GCTAATCAAGAGACAGATTGCAACTGCCCTATCCTTTTCCTAAGGGGTTGATTTACGAAGA 4043
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                                                                                                                                                  CATTGTAAATCAGACCTACAAACATATAGAGATTCTTCTGGTGAATGACGGTAGTACGGA
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       Length 19390;
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                                                                           Indels
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1.8%; Score 124.2; DB 3; llarity 50.9%; Pred. No. 4e-13; Conservative 0; Mismatches 308;
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APPLICANT: MOLLET, Beat
TITLE OF INVENTION: LACTIC BACTERIA PRODUCING
TITLE OF INVENTION: EXOPOLYSACCHARIDES
CORRESPONDENCE: 19
CORRESPONDENCE ADDRESS:
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STREET: 1155 Avenue of the Americans
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/product= "CDS (eps L) covering CDS
(eps k) on nucleotides 10392-11339"
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                      CLASSIPICATION: 426
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95201669.9
FILING DATE: 20-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: FRANCOI A., Allan
REGISTRATION NUMBER: 30256
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 14602 base pairs
TYPE: nucleic acid
STRANDEDNESS: dubble
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: CDS
LOCATION: 9285..10364
OTHER INFORMATION: /product= "epsJ"
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LOCATION: 6425..7540
OTHER INFORMATION: /product= "epsG"
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OTHER INFORMATION: /product= "epsM"
FATURE:
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LOCATION: 1807..2535
OTHER INFORMATION: /product= "epsB"
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LOCATION: 8221..9192
OTHER INFORMATION: /product= "epsI"
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OTHER INFORMATION: /product= "epsK"
EATURE:
                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: CDS
LOCATION: 352..1803
OTHER INFORMATION: /product= "epsA"
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OTHER INFORMATION: /product= "epsD'
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LOCATION: 4898..5854
OTHER INFORMATION: /product= "epsF'
                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/597,236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'PEATURE:
NAMEKTER: CDS
LOCATION: 7736.8212
OTHER INFORMATION: /product=
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OTHER INFORMATION: /product=
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LOCATION: 4051..4731
OTHER INFORMATION: /product=
                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: nisc feature LOCATION: 11302..1222 OTHER INFORMATION: (eng be FRIURE:
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10392..11339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8783 GAACAACTIACAAATIACIAAAATTGGCAAGTGAAGTGGTCTTCTTGGATGCGTATGATT 8842
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Pred. No. 8.6e-13;
0; Mismatches 358; Indels
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NAME/KEY: misc_feature
LOCATION: 13732..14305
OTHER INFORMATION: /function= "CDS on the
OTHER INFORMATION: complementary strand"
OTHER INFORMATION: /product= "orfz"
FRATURE:
NAME/KEY: terminator
LOCATION: 230..252
FRATURE:
NAME/KEY: promoter
LOCATION: 274..302
FRATURE:
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; Sequence 1, Application US/08746682A
; Patent No. 5786184
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Best Local Similarity 48.5%;
Matches 337; Conservative
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LOCATION:

US-08-597-236-1
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STATE: New TOTK

COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OFFRATING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/746,682A
FILING DATE: 14-NOV-1996
CLASSIFICATION *435
PRIOR APPLICATION NUMBER: BP 95201669.9
FILING DATE: 20-JUN-1995
APPLICATION NUMBER: BP 95201669.9
FILING DATE: 20-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAMME: FRAINCAT Allan
REGISTRATION NUMBER: 30256
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 14602 base pairs
TYPE: MODELOCK
STRANDEDNESS: double
GENERAL INFORMATION:
APPLICANT: STINGELE, Franscesca
APPLICANT: MOLLET, Beat
TITLE OF INVENTION: LACTIC BACTERIA PRODUCING
TITLE OF INVENTION: EXOPOLYSACCHARIDES
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonde
STREET: 1155 Avenue of the Americans
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LOCATION: 8221..9192
OTHER INFORMATION: /product= "eps!"
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LOCATION: 352..1803
OTHER INFORMATION: /product= "epsA"
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LOCATION: 2547..3239
OTHER INFORMATION: /product= "epsC"
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LOCATION: 3249..3995
OTHER INFORMATION: /product= "epsD"
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LOCATION: 4051..4731
OTHER INFORMATION: /product= "epsE"
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LOCATION: 4898..5854
OTHER INFORWATION: /product= "epsF"
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LOCATION: 6425..7540
OTHER INFORMATION: /product= "epsG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: 1807..2535
OTHER INFORMATION: /product= "epsB"
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OTHER INFORMATION: /product= "epsH"
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MOLECULE TYPE: DNA (genomic)
FEATURE:
                                                                                                                                                                                                                                New York
                                                                                                                                                                                                        CITY: New York STATE: New Yorl
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8423 AAAATGGTGTTGTCATCTGCACGAAATTTTGGAATTAAAAAGGCTAAAGGATCGTTTA 8482
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6598 TITICIAAAAAGCTGCTAGAGGCGGATGGTCATCGCTTTGTGGTGGCCTGTAATAAACTCT
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                                                                                                                     LOCATION: 10392..11339
OTHER INFORMATION: /product= "epsk"
PRATURE:
NAME/KEY: misc feature
LOCATION: 11302..12222
OTHER INFORMATION: /product= "CDS (eps L) covering CDS
OTHER INFORMATION: (eps k) on nucleotides 10392-11339"
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Best Local Similarity 48.5%; Pred. No. 8.6e-13;
Matches 337; Conservative 0; Mismatches 358; Indels
                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
LOCATION: 1373Z..14305
OTHER INFORMATION: /function= "CDS on the
OTHER INFORMATION: complementary strand"
OTHER INFORMATION: /product= "orfz"
NAME/KEY: CDS
LOCATION: 9285..10364
OTHER INFORMATION: /product= "epsJ"
                                                                                                                                                                                                                                                                                                                                            LOCATION: 12233..13651
OTHER INFORMATION: /product= "epsM"
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230..252
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274..302
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NAME/KEY: CDS
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US-08-746-682A-1
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5415 GCTGAATATATTATGTTTGTTGACTCTGATGATGTTGATAGTAGATTAGTAGAAAAA 5474
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Pred. No. 1.1e-12;
0; Mismatches 261; Indels
                                                                                                                                                                                                                            Sequence 1, Application US/09816028A Patent No. 6699705
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ORGANISM: Campylobacter jejuni
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54.8%;
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Best Local Similarity 54.8'
Matches 324; Conservative
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APPLICANT: Gilbert, Michel
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SEQ ID NO 1
LENGTH: 11474
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ATAAAAAAGAACTATTTGAAGATTTTCGATTTGAAAAGGGTAAGATTCATGAAGATGAAT
                                                                ACTICACTIATCGCTIGCTCTATGAGTTAGAAAAGTTGCAATAGTTAAGGAGTGCTTGT
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OTHER INFORMATION: including LOS biosynthesis locus
                                                                                                                                                                                                                                                                                                                             APPLICANT: Wakarchuk, Warren W.
APPLICANT: Wakarchuk, Warren W.
APPLICANT: National Research Council of Canada
TITLE OF INVENTION: Campylobacter Glycosyltransferases for B
TITLE OF INVENTION: Gangliosides and Ganglioside Mimics
FILE REFERENCE: 019633-000110US
CURRENT APPLICATION WUMBER: US/09/495,406
CURRENT FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: US 60/118,213
PRIOR FILING DATE: 1999-02-01
NUMBER OF SEQ ID NOS: 35
SOFTWARE: PATENTIN Ver. 2.1
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Pred. No. 1.1e-12;
0; Mismatches 261;
                                                                                                                                      6778 ACTATTATGTTGACCGAGAAAATAGTATCACAACT 6812
                                                                                                                                                             Argcctacgcacctaatagtactaat 8877
                                                                                                                                                                                                                                                           Sequence 1, Application US/09495406
Patent No. 6503744
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ORGANISM: Campylobacter jejuni
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Best Local Similarity 54.8%;
Matches 324; Conservative (
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APPLICANT: Gilbert, Michel
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US-09-495-406-1/c
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5655 6013 5177 5894 5774 5773 CACAARGAAAAAACTTAGGICTTTTAAGAGCAAGATATGAAGGTGTGAAAGTAGCAAAC 5714 APPLICANT: Wakarchuk, Warren W.
APPLICANT: Wakarchuk, Warren W.
APPLICANT: National Research Council of Canada
TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of
TITLE OF INVENTION: Gangliosides and Ganglioside Mimics
FILE REPERENCE: 019633-00011US
CURRENT APPLICATION NUMBER: US/09/816,028A
CURRENT APPLICATION NUMBER: US 60/118,213
PRIOR APPLICATION NUMBER: US 60/118,213
PRIOR PILING DATE: 1999-02-01
PRIOR PILING DATE: 2000-01-31 5654 GIGTATAAAATTTTAGATGAACAGGATGAAGTTGATTTAGTGTTTTTCAATGCTATTGT 5893 AGCTGTATCAATCAGACTTTTAAAGATATAGAAATAATTGTAGTTGATGATGTGGAAAT 5833 GATAATAGTATAAATATAGCCAAAGAATACTCTAAAAAAGACAAAAGAATAAAATAATC 4998 TAATGAGTTCTTGCCAATATTAGAGTCTTATCGAAAAGAAATACGTAGATATCCATTTAT 6132 TAAATACATCAAAATCATTTGGTAGTCTTGAATAATCAATTTCTTTTAAACTTTGGTCCAT 5058 TAAAGCGAAAAGATATTTATCAAGAAAGCATTTAGTTACGTTGTATTTGATGAAATTTTC 5118 GCCTAAACTATATGTAATGTTATAAAGAAATTTCAAAAGCAGTAGGGTAAAAATGGAT AAAATTAGTGTTATTGTTCCAGTTTATAATGTAGATAAATATTTAAGTAGTTGTATAGAA 5953 AAAATTTCAATCATCTTACCAACTTATAATGTGGAACAATATATAGAAGGGCAATAGAA AGCATTATTAATCAAAATTATAAAATATAGAAATATTATTGATAGATGATGGCTCTGTA TTATATTTTAATATTATAAAAGTAGAAGTGATTTATCTGGT-TGTTTGTACGCTACTTT 5358 TTCACT---AATCATAGTGGAGTATCAAATGCTAGAAATCATGGAATAAAGCGGAGTACA Gaps 5544 Length 11474; 9

us-09-767-041-9.rni

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TTCACT---AATCATAGTGGAGTATCAAATGCTAGAAATCATGGAATAAAGCGGAGTACA 5414
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Best Local Similarity 54.8%; Pred. No. 1.1e-12;
Matches 324; Conservative 0; Mismatches 261;
                         GCTGAATATATATGTTTGTTGACTCTGATGATGTTGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US/09/816,028
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-21
PRIOR FLILING DATE: 1999-02-01
PRIOR FILING DATE: 1999-02-01
PRIOR FILING DATE: 2000-01-31
NUMBER: OF SEQ ID NOS: 49
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                           ; Sequence 1, Application US/10303134
; Patent No. 6825019
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GENERAL INFORMATION:
APPLICANT: 0/102140.
APPLICANT: Gilbert, Michel
APPLICANT: Waterouk, Warren W.
APPLICANT: Waterouk, Warren W.
APPLICANT: Waterouk, Warren W.
APPLICANT: Wateronal Research Council of Canada
TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of
TITLE OF INVENTION: Campylobacter Glycosyltransferases
FILE REFERENCE: 019633-00011105.
CURRENT FILING DATE: 2002-11-21
FRIOR APPLICATION NUMBER: US/10/816,028
FRIOR PELLING DATE: 2001-03-21
FRIOR FILING DATE: 1999-02-01
FRIOR FILING DATE: 2000-01-31
FRIOR FILING DATE: 2000-01-31
NUMBER OF SEQ ID NOS: 49
SOFTWARRE: Patentin Ver. 2.1
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54.8%; Pred. No. 1.1e-12;
cive 0; Mismatches 261; Indels 6;
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OTHER INFORMATION: including LOS biosynthesis locus
                                                                                                                                                                                                                                                                       Sequence 1, Application US/10303162
Patent No. 6723545
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ORGANISM: Campylobacter jejuni
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Matches 324; Conservative
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APPLICANT: Gilbert, Michel
APPLICANT: Wakarchuk, Warren W.
APPLICANT: Wakarchuk, Warren W.
TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of TITLE OF INVENTION: Gangliosides and Ganglioside Mimics
FILE REFERENCE: 019633-000111US
CURRENT APPLICATION NUMBER: US/10/303,134
CURRENT FILING DATE: 2002-11-21
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OTHER INFORMATION: including LOS biosynthesis locus
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APPLICANT: Wellems, Thomas B.
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
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CACAATGAAAAAAACTTAGGTCTTTTAAGAGCAAGATATGAAGGTGTGAAAGTAGCAAAC 5714
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                                                                                          TCTCCTTATATAATGTTTTAGATCCTGATGATTATTTGGA-ACTAAATGCTTGTGAAGA
                                                                                                                                           TTATATTTTAATATTATAAAAGTAGAAGTGATTTATCTGGT-TGTTGTACGCTACTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 119.2; DB 2;
Pred. No. 3.2e-12;
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16th Floor
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FILING DATE: 10-SEP-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                Sequence 13, Application US/08487826B
Patent No. 5993827
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: 18realest, Ned
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: 01111
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-0176
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                             Sim, Kim L.
Chitnis, Chetan
Miller, Louis H.
Peterson, David S.
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nucleic acid
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe Mai
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CLASSIFICATION:
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US-08-487-826B-13
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HYPOTHETICAL:
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APPLICANT:
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4641 ACTTATACAAACATGTTGCATTCATAATTTAGAGATTATGTAATATTGTTTTTTACGT 4700 4017 TATGTTATAAAAAAAGTTATGGAGTTAATGGGGAAACAGCACTATTTTATTTTACATCA 4076 4701 AATATATATAATAATTGTTTTTTTAGTATGTATGGTATTCTAATAATATTCATAT 4760 4077 TTAGCCATATTTTTCATATATGAAACAATAGATCCGATTATTATTATTATATTAGTACTATTC 4136	4137 ITITCITCAATAGGTATTIGGAATAATATAAAAAGGATATIGGAGACAAAAAA 1196 4821 AAGTAACACAGAACATTATATATAGTAATAAATAGAAGAAATAATATTITTATGTTAT 4880 4197 GAATGATTTAATTICAGTTATTGTACCAATTTATATATGCCAAGATTATCTTGATAATG 4256 4197 GAATGATTTAATTICAGTAATTATATATATATCTCAAGATTATCTTGATAATG 4256 4187 GAATGATTAATATATAAAGGGGAAAATTCATAATATATAT		# ### ################################	4492 TTCGAGAGAATGCATGATAATATAACTGAGTATAATGCCGATATAGCAGAGATTTT 4551	4612 ACGAGAGAGACTGTAAAAGAATTTTTGTCAGGATCTAATATAGA 4658 		4837 CTTATTAATCAGAAATTCTCTATAAATAATTATTGATTTAGTCACAAGATTGGAGAATTAC 4896 5541 TTGAAAATATTTAAATAATAATAATAATAATTAGTTAAAATAAT	4957 GTTAAATGTTTAAACAAATGTATTCAACAGATTGTTTGGATAATGAGTTCTTGCCAATA 5016

5435 6195 5555 6255 6615 5956 5556 GAAGTGAATAATCCAAATATTGAAGCAATTAATACCGTGCAGGACATGGGAGAA 5615 5077 T-CAAGAAAGCATTTAGTTACGTTGTATTTGATGAAATTTTCGCCTAAACTATATGTAAT 5135 5780 İGCATTACAĞTTAAGGGİTTATAGİTİTİTİTİTTİTİTİTTACATATATATAAAAA 5839 5316 IGCAAGGAATATGCAGAAAAAAAAAAAAGAGTAAAAATTTTTTCACTAATCATAGTGGA 5375 6316 TTTTACTTATTTTTTTTATACATAAATTTTGAAATTCATAAAATGCATGAAATA 6375 6616 aaarargaragaraararagagagagaaacgaagaacarararrercrerringrara 5975 GITTAAATACGGAAAACAGTCTATTTTTGACAATTTTTTAATTTTTAGAAATCTTTATAA 6034 6035 AAAATATTATTTTAACTTGTTAAAAGTATCTAACAAAAATTCTTTGTCTAAAAATTTTG 6094 6095 TATAAGAATTGTTTCGAACAAGTTTTTAAAAAATATATTATGGTTATAATAGGAAGATAT 6154 5675 TAAGAAAAGATACATAACAGATCTTTTCAAGAGAATCAATGGTTAGGAGAAGATTTACT 5734 5795 TITITATAGGAGAGGTATACTAAGTACAGTAAATTCTTTTAAAGAAGGTGTGTTTTTGCA 5854 5855 ATTGGAAAATTTGCAAAAACAAGTGATAGTATTGTTTAAGCAAATATATGGTGAGGATTT 5914 5915 TGACGTATCAATTGTTAAAGATACTATACGTTGGCAAGTATTTTATATAGCTTACTAAT 5974 GTTATATAAGAAATTTCAAAAGCAGTAGAGGTAAAAATGGATAAAATTAGTGTTATTGTT 5196 CCAGTTTATAATGTAGATAATATTTAAGTAGTTGTATAGAAAGCATTATTAATCAAAAT 5900 TATATATAAA---GACATTAAAACTATACTAATAGGTAATTAGTTTTATTATATCATCCT 5256 TATAAAATATATAGAAATATTATTGATAGATGATGGCTCTGTAGATGATTCTGCTAAAATA 6136 TACTATTTTATACATGCATTTTTATATATTTTAGTATATACTTTAAAGGTATATTAAT 5496 AGTAGAAGTGATTTATCTGGTTGTTTGTACGCTACTTTTTCAGAAAATATAAATTTT

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6155 CATGGATACT - - ATTAGTAAAATTTCTATAATTGTACCTATATATAATGTAGAAAATAT 6212
           6213 TTATCTAAATGTATAGATAGCATTGTAAATCAGACCTACAAACATATAGAGATTCTTCTG 6272
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Search completed: April 28, 2005, 15:47:29 Job time : 1118 secs

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April 28, 2005, 14:17:37 ; Search time 3571 Seconds (without alignments) 11919.659 Million cell updates/sec
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Sequence 29, Appl
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Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-767-041-29

US-09-900-038A-3

US-10-865-873-3

US-09-870-759-83

US-09-870-759-83

US-09-871-708A-83

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Maximum Match 1008
Listing first 45 summaries
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seq length: 200000000
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Maximum DB
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171, App
172, App
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sequence 170, App
Sequence 175, App
Sequence 1, Appl
Sequence 1, Appl
Sequence 178, App
Sequence 179, App
Sequence 179, App
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Sequence 1, Appli
Sequence 26, Appl
Sequence 26, Appl
Sequence 23, Appl
Sequence 132, Appl
Sequence 214, Ap
Sequence 38093, A
Sequence 175, Appl
Sequence 27, Appl
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APPLICANT: Smith, Hilda
TITLE OF INVENTION:
FILE REFERENCE: 2183-4726
CURRENT APPLICATION NUMBER: US/09/767,041
CURRENT FILING DATE: 2001-01-22
PRIOR PAPLICATION NUMBER: PCT/NL99/00460
PRIOR APPLICATION NUMBER: BP8202465.5
PRIOR APPLICATION NUMBER: BP8202465.5
PRIOR APPLICATION NUMBER: BP8202467.1
PRIOR FILING DATE: 1998-07-22
PRIOR FILING DATE: 1998-07-22
NUMBER OF SEQ ID NOS: 53
SOFTWARE: Patentin version 3.0
SEQ ID NO 9
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Sequence 177,
Sequence 386,
Sequence 386,
Sequence 240,
Sequence 240,
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US-10-329-676-18

US-10-240-453-26

US-10-706-635-23

US-10-706-635-23

US-10-240-453-132

US-10-231-228-38939

US-10-808-1228-38939
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B US-10-804-408-162
B US-10-804-408-173
B US-10-804-408-171
B US-10-804-408-168
B US-10-804-408-168
B US-10-804-408-165
B US-10-804-408-165
B US-10-804-408-170
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Patent No. US20020055168A1
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LOCATION: (1)...(6992)
COTHER INFORMATION: CPS
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Sequence 3, Sequence 83,

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Patent No. US20020055168A1

GENERAL INFORMATION:
TITLE OF INVENTION:
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/09/767,041

CURRENT APPLICATION NUMBER: PCT/NL99/00460

PRIOR APPLICATION NUMBER: PP98202465.5

PRIOR PILING DATE: 1998-07-22

PRIOR FILING DATE: 1998-07-22

PRIOR PILING DATE: 1998-07-22

PRIOR FILING DATE: 1998-07-22

PRIOR FILING DATE: 1998-07-22

NUMBER OF SEQ ID NOS: 53

SOFTWARE: PatentIn version 3.0

SEQ ID NO 29

LENGTH: 6992
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                   GTAAAAAGCTGCTAGAAGGGGGATGGTCATCGCTTTGTGGTGGCCCTGTAATAAACTCTATA
                                                     AAAAAGAACTATTGAAGATTTTCGATTTGAAAAGGGTAAGATTCATGAAGATACT
                                                                    AAAAAGAACTATTTGAAGATTTTCGATTTGAAAAGGGTAAGATTCATGAAGATGAATACT
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OTHER INFORMATION: CPS1
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                                                                    APPLICANT: Wiyake, Katsuhide
APPLICANT: Wiyake, Katsuhide
APPLICANT: Watanabe, Masaki
APPLICANT: Watanabe, Masaki
APPLICANT: Watanabe, Masaki
APPLICANT: Injima, Shinji
TITLE OF INVENTION: Beta 1,3-galactosyltransferase and DNA encoding the
FILE REFERENCE: 766.53
CURRENT APPLICATION NUMBER: US/10/865,873
CURRENT FILING DATE: 2004-06-14
PRIOR PILING DATE: 2001-07-09
PRIOR FILING DATE: 2001-01-05
PRIOR FILING DATE: 2001-01-05
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.0
SSEQ ID NO.3
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Pred. No. 9.1e-93;
0; Mismatches 917; Indels
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                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Streptococcus agalactiae type
US-10-865-873-3
; Sequence 3, Application US/10865873
; Publication No. US20050064559A1
; GENERAL INFORMATION:
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NAMB/KRY: CDS
: LOCATION: (3982)..(4953)
: FEATURE:
NAMB/KEY: CDS
: LOCATION: (5009)..(5947)
US-10-865-873-3
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                                                                                                                                                                                                                  Score 726.8; DB 9;
Pred. No. 1.7e-92;
0; Mismatches 902;
                                                                                                                                                                                                                      10.4%;
59.2%;
    SOFTWARE: PatentIn version 3.1
SEQ ID NO 83
LENGTH: 17276
TYPE: DNA
                                                                                                                                                                                                                  Query Match
Best Local Similarity 59.2
Matches 1366; Conservative
                                                                            ORGANISM: Streptococcus FEATURE:
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                                                                                                                                    ; LOCATION: (7062).
; OTHER INFORMATION
US-09-870-759-83
                                                                                                                     NAME/KEY: CDS
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Patent No. US2002017551A1
GENERAL INFORMATION:
APPLICANT: TERMAN, David S
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
CURRENT APPLICATION NUMBER: US/09/870,759
CURRENT FILING DATE: 2002-01-14
PRIOR FILING DATE: 2000-05-30
NUMBER OF SEQ ID NOS: 166
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	90 ATAICCTAAATCTATTAACTTGGGGAGTATTTTTTAATGATTTTTTGTAACAGTAACAGTAGGAACT 184
0y 1	1847 CATGAACAACAGTTTAATCGAFTGATAAAAGAGATTGATTTATTGAAAAAAAAAA
op qa	6616 CATGAACAGCAGTTCAACCGTCTTATTAAAGAAGTTGATAGATTAAAAGGGACAGGTGCT 6675
Oy 1	1907 ATAACCGAGGAATATTTATTCAAACAGGATATTCTGACTATATTCCAGAATATTGCAAG 1966
	7 TATAAAAAATTTCTCAGTTACAAAGAAATGGAACAATATATTAACAAATCAGAAGTAGTT 202
9 qa	6736 TGGTCAAAATTTCTCTCATATGATGATATGAACTCTTACATGAAAGAAGCTGAGATTGTT 6795
2	2027 ATTIGCCACGGAGGCCCGCTACTTTTAFGAATTCATTATCCAAAGGAAAAAAAAATTA 2086
9 qu	6796 ATCACACACGCGCCCCAGCGACGTTTATGTCAGTTATTTCTTTAGGGAAATTACCAGTT 6855
0y 2	2087 TIGITICCTAGACAAAAAAGTAIGGGAACAIGIAAATGAICAICAAGTAGAGTITGIA 2146
op qu	6856 giteriteciaggagaaagecagiritggigaacararcaargarcarcaarararriia 6915
	agaagaattitacaagaiaataatatttatttatatagaaaatatagatgattgaa 220
	6916 AAAAAAATTGCCCACCTGTATCCCTTGGCTTGGATTGAAGATGTAGATGGACTTGCGGAA 6975
7	2207 AAAAITAITGAAGIITCIAAGCAAACTAACIITACAICAAATAAIAAITTITITITGIGAA 2266
Db da	6976 gegitgaaaagaatatagetacagaaaaatatcaggaaataatgatatgittigicat 7035
0y 2	2267 AGATTAAAACAAATAGTTGAAAAATT 2292
Dp 1	7036 AAATTAGAAAATTATAGGTGAAAT 7061
RESULT 7 US-10-428- ; Sequence ; Publicat ; GENERAL ; APPLICA ; TITLE O	RESULT 7 US-10-428-817A-79 ; Sequence 79, Application US/10428817A ; Sequence 79, Application US/10428817A ; Gublication No. US20040214783A1 ; GENERAL INFORMATION: ; APPLICANT: TERMAN, David S ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE ; FILE REFERENCE: 38373-189118

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TAAAGTTAGATGTTCAATAATGAATGAATGGTCTATTTGGTCAGATATTAAGATTATTAC 6075
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            3362 AATACCAAATACAAGATATTATTAATGACATTGAAGCAATGGGAGTGATTGTCAATGTTA 5421
                                                                                        ATGTAGAGGCACTTAGCTTTGATAATATAGGAGAAAAGCGAATCCAAACTTTTGAAGGAT 5481
                                                                                                                                                                       ATAGTGTTATTACATATTCTATGAATTCTATAAATATAGTCACCTTATAGCAAAACGAT 5541
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Pred. No. 1.7e-92;
0; Mismatches 902; Indels
CURRENT APPLICATION NUMBER: US/10/428,817A
CURRENT FILING DATE: 2003-05-05
PRIOR PAPLICATION NUMBER: US 60/378,988
PRIOR FILING DATE: 2002-06-08
PRIOR APPLICATION NUMBER: US 60/389,366
PRIOR PILING DATE: 2002-06-15
PRIOR APPLICATION NUMBER: US 60/406,697
PRIOR APPLICATION NUMBER: US 60/406,750
PRIOR PILING DATE: 2002-08-28
PRIOR FILING DATE: 2002-08-28
PRIOR FILING DATE: 2002-08-19
PRIOR PILING DATE: 2002-10-01
PRIOR PILING DATE: 2002-10-01
PRIOR PILING DATE: 2002-10-02
PRIOR PELING DATE: 2002-10-02
PRIOR APPLICATION NUMBER: US 60/415,400
PRIOR PILING DATE: 2003-10-02
PRIOR PILING DATE: 2003-10-02
PRIOR APPLICATION NUMBER: US 60/415,400
PRIOR APPLICATION NUMBER: US 60/415,400
PRIOR APPLICATION NUMBER: US 60/438,686
PRIOR APPLICATION NUMBER: US 60/438,686
PRIOR SEQ ID NOS: 224
NUMBER OF SEQ ID NOS: 224
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Best Local Similarity 59.2%;
Matches 1366; Conservative
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; NAME/KEY: CDS
; LOCATION: (7062)..(8207)
US-10-428-817A-79
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                                                                         TITIAICITICIGATITITIACAGAGACITITIGAGGICGIGGCIATCITIGAAGAGITIAAA
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CTCCCAATTTTAAAAGCAATAAAGATTTATTGTTTGTTCTAATTGATACATTATATTGTC
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Publication No. US20040009574A1
GENERAL INFORMATION:
APPLICANT: Dategupte, Nanibhushan
APPLICANT: Stah, Ketan
TITLE OF INVENTION: GENERAL
FITTE OF INVENTION: GENERAL
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Pred. No. 1.1e-91;
0; Mismatches 926; Indels
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Best Local Similarity 58.9%;
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OY 2263 TGAAAGATTAAAACAATAGATGAAAAATTTAATGAGGATCAAGAAAATGAATAATAAAA 2322	SULT 9 10-461-990-4 Sequence 4, Application US/10, Publication No. US20040023361J PAPLICANT: Nestec, S.A. APPLICANT: Nestec, S.A. APPLICANT: Stingele, France APPLICANT: Stingele, France APPLICANT: Stingele, France APPLICANT: Stingele, France APPLICANT: Stingele, France APPLICANT: Stingele, France APPLICANT: Stingele, France APPLICANT: Stingele, France APPLICANT: Stingele, France APPLICANT: Stingele, France TILE OF INVENTION: Lactic ACTILE OF INVENTION: Lactic ACTILE OF INVENTION NUMBER: UCURRENT APPLICATION NUMBER: DERIOR PRIOR APPLICATION NUMBER: DERI	Qy 798 GGAGCGGTAGTCGGGTTAATTTTGTGGTATAGTTTTTTTT
1203 GGGATTACAGGTCTCTGGCAGGTTAGTGGTCGTAATATCACAGACTTCGACGACGTA 1262	6406 GTRANGTHOGHTCANTATATATATATATATATATATATATATATATATATA	7245 TGIGGTTCCTAGACAGAACAGTTTGAGTGTTGAATAATCATCGGGGGTGTTTTTT 7304 2146 AAGAAGAATTTTACAGATAATAATATTTTATTTATAGAAAATAGATGTTGTTTGA 2205 2146 AAGAGTTTTCTGAAAATTGAATTTGATTTTGAATATCAGTGATTTGTTTG

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 2226;
APPLICANT: GILBERT, GWENDOLYN
TITLE OF INVENTION: MOLECULAR TYPING OF GROUP B STREPTOCOCCI
FILE REFERENCE: 675002-2001
CURRENT APPLICATION NUMBER: US/10/804,408
CURRENT FILING DATE: 2004-03-19
FRIOR APPLICATION NUMBER: PCT/AU02/01281
PRIOR FILING DATE: 2002-09-18
PRIOR FILING DATE: 2002-09-18
PRIOR PILING DATE: 2001-09-19
NUMBER OF SEQ ID NOS: 182
SOFTWARE: Patentin version 3.2
SSOFTWARE: Patentin version 3.2
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Pred. No. 2.6e-82;
0; Mismatches 791; Indels
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Best Local Similarity
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US-10-804-408-166
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Sequence 166, Application US/10804408 Publication No. US20040253617A1 GENERAL INFORMATION: APPLICANT: FANRONG, KONG

RESULT 10 US-10-804-408-166

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242 CTCCCAATTTTAAAAGCAATAAAGATTTATTGTTTGTTCTATTGATACATTATATTGTCT
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                                                                       ATAACCGACGAAATATTTATTCAAACAGGATATTCTGACTATATTCCAGAATATTGCAAG
                                                                                                                 2153 TGGTCAAAATTTCTCTCATATGATGATATGAACTGTTACATGAGAAGAGCTGAGATTGTT
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Publication No. US20040253617A1

GENERAL INFORMATION:
APPLICANT: FANRONG, KONG

TILLE OF INVENTION: MOLECULAR TYPING OF GROUP B STREPTOCOCCI
FILE REPERBNCE: 675002-2001
CURRENT FILING DATE: 2004-03-19

PRIOR APPLICATION NUMBER: PCT/AU02/01281

PRIOR APPLICATION NUMBER: PCT/AU02/01281

PRIOR APPLICATION NUMBER: DCT/AU02/01281

PRIOR APPLICATION NUMBER: DCT/AU02/01281

PRIOR PILING DATE: 2002-09-18

PRIOR PILING DATE: 2002-09-18

PRIOR PILING DATE: 2001-09-19

NUMBER OF SEQ ID NOS: 182
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Pred. No. 2.6e-82;
0; Mismatches 791;
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ilarity 59.6%;
Conservative
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Best Local Similarity
Matches 1225; Conserv
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                                       TITICGATATCATGGGTGCTATTATAGGTTTGCTCATATGTGGCATTGTGGCAATTTTTC 1018
                                                                                                                        TAGTTCCGCAAATCAGAAAAGATGGTGGACCGGCTATCTTTTCTCAAAATAGAGTAGGTC 1078
                                                                                                                                                                                                                                       GTAATGGTAGGATTTTTAGATTCTATAATTCAGATCAATGCGAGTAGATGCAGAACAAA 1138
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TTTTGGATATACTCGGAGCGGTAGTCGGGTTAATTATTTGTGGTATAGTTTCTATTTTGT
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0; Mismatches 792; Indels
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APPLICANT: GILBERT, GWENDOLYN
TITLE OF INVENTION: MOLECULAR TYPING OF GROUP B S;
FILE REFERRINCE: 675002-2001
CURRENT APPLICATION NUMBER: US/10/804,408
CURRENT PILING DATE: 2004-03-19
PRIOR APPLICATION NUMBER: PCT/AU02/01281
PRIOR PLING DATE: 2002-09-18
PRIOR FILING DATE: 2001-09-19
PRIOR FILING DATE: 2001-09-19
PRIOR FILING DATE: 2001-09-19
NUMBER OF SEQ ID NOS: 182
SOFTWARE: PATENTIN VERSION 3.2
SOFTWARE: PATENTIN VERSION 3.2
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                                                                                                                                                             Gaps
                                                                                                                                      DB 18; Length 2226;
                                                                                                                                                             38;
                                                                                                                                     Score 649.2; DB 18; Length
Pred. No. 7.3e-82;
0; Mismatches 793; Indels
                                                                                                   OTHER INFORMATION: Consensus sequence US-10-804-408-173
PRIOR APPLICATION NUMBER: AU PR 7749
PRIOR FILING DATE: 2001-09-19
NUMBER OF SEQ ID NOS: 182
SOFTWARE: PatentIn version 3.2
SEQ ID NO 173
LENGTH: 2226
                                                                                                                                     Query Match

9.3%;
Best Local Similarity 59.5%;
Matches 1223; Conservative 0
                                                                            ORGANISM: Artificial Sequence
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Qy 553 TITCAACAAGGA Db 719 AGTTAACCTGCTT Qy 610ACGTAAA	Db 779 AATACCAAATACA Qy 664 ATATTAATTCATT		Qy 784 TTTTGGATATACT Db 959 TTTTGGATATCAC Qy 844 TAGTTCCAATTAT	Db 1019 TAGHTCCACAATT Qy 904 AGAATGGACGCATT Db 1079 GTAATGGTAGGAT		1024	1253	1313	Db 1373 GAATCACTGTTT 1373 GAATCACTGGTTT 1364 HERSCHIMMAGAAGTTT	1433	1324 IAAAG 1493 TCCTA	1374	1613	1673	Cy 1547 CALTANITIACIO
2093 1967 2153	Qy 2027 ATTTGCCACGAGG 2040 Db 2213 ATCACACATGGCGG 2226	RESULT 14 US-10-804-408-171 ; Sequence 171, Application US/10804408 ; Publication No. US20040253617A1 ; GENERAL INFORMATION . A DEPTICATION OF WARRAL OF TAXABLE TO T	APPLICANT: FARKONS, NOWS, APPLICANT: GLIBERT, WENDOLYN TITLE OF INVENTION: MOLECULAR TYPING OF GROUP B STREPTOCOCCI FILE REFERENCE: 675002-2001 CURRENT APPLICATION NUMBER: US/10/804,408 CURRENT FILING DATE: 2004-03-19 DP10R APPLICATION NUMBER: DCT/A102/01281	PRIOR FLING DATE: 2002-09-18 PRIOR PLLING DATE: 2002-09-18 PRIOR FLING DATE: 2001-09-19 NUMBER OF SEQ ID NOS: 182 SOFTWARE: Patentin version 3.2	; SEC ID NO 171 ; LENGTH: 2226 ; TYPE: DNA ; ORGANISM: Streptococcus agalactiae US-10-804-408-171	Query Match 9.3%; Score 648.8; DB 18; Length 2226; Best Local Similarity 59.5%; Pred. No. 8.3e-82; Matches 1222; Conservative 1; Mismatches 793; Indels 38; Gaps 6;	Qy 16 IGGCATTATTTGATATGATAGCAGTTGCAATTTCTGCAATCTTAACAAGTCATATACCAA 75	Qy 76 AIGCIGAITIAAAICGTICIGGAATTITIAICATAAIGAIGGITCAITAITITIGCAI 132 Db 242 CICCCAAYITIAAAAGCAAIAAAGAITIAITGITIGTITGAIAGAITAIAITGICI 301	OY 133 TITITATATCTCGTATGCCAGTTGAATTTGAGTATAGAGGTAATCTGATAGAGTTTGAAA 192 DD 302 TITATCTTTCTGATTTTTAGAGACTTTTGGAGTCTGGGCTATCTTGAAGAGTTTAAAA 361	Oy 193 AAACATTTAACTATAGTATAATATTTGCAATTTTTCTTACGGCAGTATCATTTTGTTGG 252 Db 362 TGGTATTGAAATACAGCTTTTACTATATTTTCATATCAAGTTCATTTTTTTT	Qy 253 AGAATAATTTGGCACTTTCAAGACGTGCTGCTGTATTTCACATTAATAAACTTCGTTT 312	Qy 313 TGGTATACCTATTTAACGTAATTATTAAGCAGTTTAAGGATAGCTTTCTATTTTCGACAA 372	OY 373 TCTATCAAAAAAAGAGGATTCTAATTACAAGGCTGAACGATGGGAAAATÀTGCAAGTTT 432 DD 542 CACGAGATACCAAAGTTGTTTTGATAACGATTACTTTATCAAAATGACCTTTA 601	Qy 433 TATTIGAATCACAAAATTCAAAAAATCTIGTIGCATIGGTAGTITITAGGTACAG 492 Db 602 GGAATAAATACGACCATAATTATATGCTGTATCTTGGATTCCTCTGAAAAGG 658	Oy 493 AAATAGATAAAATTAATCATTACCGCTCTATTATTCTGTGGAAGAGCTATAGAGT 552 DD 659 ATTGTTATGATTTGAAACATAACTCGTTAAGGATAAAAAAAA

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TTGGAAGGAAGAAGGTTTTTGGGTAACATTTGATAAAGAGGATGC 1486
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	253 AGAATAATTTCGCACTTTCAAGACGTGGTGCCGTGTATTTCACATTAATAAACTTCGTTT 312	313 TGGTATACCTATTTAACGTAATTATAAGCAGTTTAAGGATAGCTTTCTATTTCGACAA 372 	373 TCTATCAAAAAAGACGATTCTAATTACAACGGCTGAACGATGGGAAAATATGCAAGTTT 432 	433 TATTTGAATCACATAAAAAATTCAAAAAATCTTGTTGCTATTGGTAGTTTTAGGTACAG 492	493 AAATAGATAAAATTAATTTATCATTACCGCTCTATTATTCTGTGGAAGAAGCTATAGAGT 552	553 TTTCAACAAGGGAAGTGGTCGACCACTCTTTATAAATCTACCAAGTGAGTTTTTAG 609	610ACGTAAAGCAATTCGTTTCAGATTTTGAGTTGTTAGGTATTGATGTAAGCGTTG 663 	664 ATATTAATTCATTCGGTTTTACTGCGTTGAAAACAAAAAAATCCAACTGGTGGCC 723 	724 ATAGCATTGTAACTTTTTCCACAAATTTTTATAAGCCTAGTCATATCATGAAAGGAC 783 	784 ITITGGATATACTCGGAGCGGTAGTCGGGTTAATTTGTGGTATAGTTTCTGT 843 	844 TAGTICCAATTAITGGTAGAGGTGGACGGGGTAITTITGCICAGAAAGGGGTTGGAC 903 	904 AGAATGGACGCATATTTACATTCTACAAGTTTCGATGTATGT	964 GCAAAAAAGACTTGGTCAGCCAAAACCAGATGCAAGGGTGGGT	1024 AAACGATCCTAGAATTACTCCAATTGGACATTTCATACGCAAAAACAAGTTTAGACGAGT 1083 	1084 TACCACAGTITTATAAGTITTAATIGGCGATATGAGTCTAGTIGGTACACGTCCACCTA 1143 	1144 CAGITGATGAAITICAAAAATATACICCIGGICAAAAGGAGGAGGAITGAGITITAAACCAG 1203 	1204 GGATTACAGGTCTCTGGCAGGTTAGTGGTCGTAGTAATATCACAGACTTCGACGACGTAG 1263 	1264 TTCGGTTGGACTTAGCATACATTGATAATTGGACTATCTGGTCAGATATTAAAATTTAT 1323
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                            APPLICANT: FANKONG, KONG
APPLICANT: FANKONG, KONG
TITLE OF INVENTION: MCLECULAR TYPING OF GROUP B STREPTOCOCCI
TITLE OF INVENTION: MCLECULAR TYPING OF GROUP B STREPTOCOCCI
CURRENT APPLICATION NUMBER: US/10/804,408
CURRENT FILING DATE: 2004-09-19
PRIOR APPLICATION NUMBER: PCT/AU02/01281
PRIOR APPLICATION NUMBER: PCT/AU02/01281
PRIOR APPLICATION NUMBER: AU PR 7749
PRIOR FILING DATE: 2001-09-19
PRIOR FILING DATE: 2001-09-19
NUMBER OF SEQ ID NOS: 182
SOFTWARE: PatentIn version 3.2
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Publication No. US20040253617A1
GENERAL INFORMATION:
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                                                                                                                Length
                                                                                                             Score 647.6; DB 18; Length
Pred. No. 1.2e-81;
0; Mismatches 794; Indels
; TYPE: DNA
; ORGANISM: Streptococcus agalactiae
US-10-804-408-168
                                                                                                          Query Match 9.3%;
Best Local Similarity 59.5%;
Matches 1222; Conservative
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; Sequence 169, Application US/10804408; Publication No. US20040253617A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Streptococcus agalactiae
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                                                                 1194 CGATGATCCTAGAATTACTAAAATAGGAAAATTTATTCG-AAAAACAAGCATAGATGAGT
                                                                                        TACCACAGTTTTATAATGTTTTAATTGGCGATATGAGTCTAGTTGGTACACGTCCACCTA
                                                                                                                                     CAGTTGATGAATTTTGAAAATATATACTCCTGGTCAAAAGAGACGATTGAGTTTTAAACCAG
                                                                                                                                                            CAGTIGATGAATATGAAAGTATAATTCAACGCAGAAGCGACGCCTTAGTTTTAAGCCAG
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Pred. No. 1.2e-81;
0; Mismatches 794; Indels
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                                                                     GROUP
APPLICANT: FANRONG, KONG
APPLICANT: FANRONG, KONG
TITLE OF INVENTION: MOLECULAR TYPING OF GROU
CURRENT APPLICATION NUMBER: US/10/804,408
CURRENT FILING DATE: 2004-03-19
PRIOR PELING DATE: 2002-09-18
PRIOR PLING DATE: 2001-09-19
PRIOR PLING DATE: 2001-09-19
PRIOR PLING DATE: 2001-09-19
SEGIND NOS: 182
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Pred. No. 2e-81;
0; Mismatches 795;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 164, Application US/10804408
| Publication No. US20040253617A1
| GENERAL INFORMATION:
| APPLICANT: FANRONG, KONG
| APPLICANT: GILBERT, GWENDOLYN
| TITLE NE FERENCE: 675002-2001
| CURRENT APPLICATION NUMBER: US/10/804,408
| CURRENT APPLICATION NUMBER: PCT/AU02/01281
| PRIOR PILING DATE: 2004-03-19
| PRIOR FILING DATE: 2002-09-18
| PRIOR FILING DATE: 2001-09-19
| NUMBER OF SEQ ID NOS: 182
| SOFTWARE: PATCHING DATE: 2001-09-19
| NUMBER OF SEQ ID NOS: 182
| SOFTWARE: PATCHING DATE: 2011-09-19
| SOFTWARE: PATCHING DATE: 2011-09-19
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Matches 1221; Conservative
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Pred. No. 3.4e-81;
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Publication No. US20040253617A1
GENERAL INPORMATION:
JAPELICANT: FARRONG, KONG
TITLE OF INVENTION: MOLECULAR TYPING OF GROUP B STILE REFERENCE: 675002-2001
CURRENT APPLICATION NUMBER: US/10/804,408
CURRENT FILING DATE: 2004-03-19
PRIOR APPLICATION NUMBER: PCT/AU02/01281
PRIOR APPLICATION NUMBER: AU PR 7749
PRIOR PILING DATE: 2001-09-19
PRIOR FILING DATE: 2001-09-19
NUMBER OF SEQ ID NOS: 182
SOFTWARE: Patentin version 3.2
SEQ ID NO 163
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Matches 1220; Conservative 0; Mismatches 796; Indels 38; Gaps 6;	16 TGGCATTATTTGATATGATAGCAGTTGCAATTTCTGCAATCTTAACAAGTCATATACCAA 75	1/3 IACCGAICATTICAMACAGITGIGGITTATOTTTTATCATAGATTIGACATTATTTATCG 232	233 CTCCCAATTTTAAAAGCAATAAGATTTATTGTTTGTTCTATTGATACATTATATTTTTT 292	133 TTTTATATATCTCGTATGCCAGTTCAATTTGAGTATAGAGGTAATCTGATACAGTTTGAAA 192 293 TTTATCTGATTTTTACAGAGCTTTTGGAGTGTGGCTATCTTGAAGAGTTTAAAA 352	193 AAACATTTAACTATAGTATAATATTTGCAATTTTTCTTACGGCAGTATCATTTTTGTTGG 252	AGABTAATTTCGCACTTTCTAGACGTGGTGTATTTCAGATTAATAACTTCGTTT	AAAACTCTT	313 IGGTATACCTATTTAACGTAATTATTAAGCAGTTTAAGGATAGCTTTCTATTTTCGACAA 372 	373 TCTATCAAAAAAAGACGATTCTAATTACAACGGCTGAACGATGGGGAAAATATGCAAGTTT 432	III.CACGAGAIACCCAAAGIIGIIIIGAIAACGAAAAAATCTTGTTGCATTGGTAGTTTTAGGTACAGGTACAGGTACATTAGGTACAGGTACAGGTACAGGTACAGGTACAGGTACAGGTACAGGTACAGGTACAGGTACAGGTAGGT	TTAGGAACAAATACGACCATAATTATATCGCTGTCTGTATCTTGGACTCCTCTGAAAAG	493 AAATAGATAAATTATCATTACCGCTCTATTATTCTGGGAAGAAGCTATAGAGT 552 	553 TITCAACAAGGGAAGTGGTCGACCACGTCTITATAAATCTACCAAGTGAGTTTTTAG 609 		770 AATACCAAATACAAGATATTATTGACATTGAAGCAATGGGAGTGATTGTCAATGTTA 829 664 ATATTAATTCATTGGGTTTTACTGGGGTTGAAAAAAAAAA		724 ATAGCATTGTAACTTTTTCCACAAATTTTTATAAGCCTAGTCATATCATGAAGGAC 783 	784 ITTIGGATATACTCGGAGCGGTAGTCGGGTTAATTATTTGTGGTATAGTTTTCTATTTTGT 843			GTAATGGTAGGATTTTTAGATTCTATAAATTCAGATCAATGCGAGTAGATGCAGAAA	964 GCAAAAAAACTIGCICAGCCAAAACCAGAIGGGIGGGIGGGITITITAAAAIGGGAA 1023 1130 TTAAGAAAGATITATTAGTICACAAICAAATGACGGCTAAIGTITAAGTIAGA 1184	1024 AAACGATCCTAGAATTACTCCAATTGGACATTTCATACGCAAAAACAAGTTTAGACGGT 1083
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                                                    STREPTOCOCCI
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Publication No. US20040253617A1
GENERAL INFORMATION:
APPLICANT: FANRONG, KONG
APPLICANT: FANRONG, KONG
TITLE OF INVENTION: MOLECULAR TYPING OF GROUP B S; FILE REFERENCE: 67502-2001
CURRENT APPLICATION NUMBER: US/10/804,408
CURRENT FILING DATE: 2004-03-19
PRIOR APPLICATION NUMBER: PCT/AU02/01281
PRIOR APPLICATION NUMBER: AD PRIOR APPLICATION NUMBER: AD PRIOR FILING DATE: 2001-09-18
PRIOR FILING DATE: 2001-09-19
NUMBER OF SEQ ID NOS: 182
SOFTWARE: PATENTIN VERSION 3.2
SOFTWARE: PATENTIN VERSION 3.2
                                                    В
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                                                                                                                                                                                               TYPE: DNA
ORGANISM: Streptococcus agalactiae
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Matches 1220; Conservative
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US-10-804-408-170
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GGATTACAGGTCTCTGGCAGGTTAGTGGTCGTAGTAATATCACAGACTTCGACGACGTAG 1263
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                                                                                                                            659 ATTGTTATGATTTGAAACATAACTCGTTAAGGATAATAAACAAGATGCTCTTACTTCAG
                                                                                                                                                                53 TTTCAACAAGGGAAGTGGTCGACCACGTCTTTATAAATCTACCAAGTGAGTTTTTAG---
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                                                                       CATGAACAGCAGTTCAACCGTCTTATTAAAGAAGTTGATAGATTAAAAAGGGACAGATGCT
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Pred. No. 2.1e-80;
0; Mismatches 792; Indels
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APPLICANT: FANKONG, KONG
TITLE OF INVENTION: MOLECULAR TYPING OF GROUP B S
FILE REFERENCE: 675002-2001
CURRENT APPLICATION NUMBER: US/10/804,408
CURRENT FILING DATE: 2004-03-19
PRIOR APPLICATION NUMBER: PCT/AU02/01281
PRIOR APPLICATION NUMBER: AU PR 7749
PRIOR PILING DATE: 2001-09-19
NUMBER: OF SEQ ID NOS: 182
SOFTWARE: Patentin version 3.2
SSEQ ID NO 1655
                                                                                                                                                                                                                                                                                                                                                                                  Sequence 165, Application US/10804408
Publication No. US20040253617A1
GENERAL INFORMATION:
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Best Local Similarity 59.5%;
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                                                                                                                                                                                                                                                                                                                                              Score 428.4; DB 16;
Pred. No. 1.3e-50;
0; Mismatches 581;
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Best Local Similarity 58.9<sup>3</sup>
Matches 849; Conservative
 CDS
(1809)..(2501)
                                                                                                         CDS (3332)..(4015)
                                                                                                                                                                                                                                                                      ; NAME/KEY: CDS
; LOCATION: (5687)..(6778)
US-10-182-960-1
                                                                         (2618)..(3307)
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1487 AAGAAGTCTTTTGAAGAATGAAAAATGTATCCATGTTACTTTCCAACAAATCGCAATCT
                                                                    CATTAATTTAGTGAAAAATACTTTCTTAGCTTTCAAAATTTTACGTGATGAGAAACCAGA
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                                  1672 TAGGAGTATTCTAAGAGAGAGTTGTATATCATTGCTTCTTTCCAACAACAAATGT
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TITLE OF INVENTION: Biopolymer Thickner
FILE REFRENCE: 6437
CURRENT PEPLICATION NUMBER: US/10/182,960
CURRENT FILING DATE: 2002-08-03
PRIOR APPLICATION NUMBER: CFT/US01/03404
PRIOR FILING DATE: 2001-02-02
PRIOR FILING DATE: 2000-10-16
PRIOR FILING DATE: 2000-10-16
PRIOR PILING DATE: 2000-02-02
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
LENGTH: 6850
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Publication No. US20030186392A1
GENERAL INFORMATION:
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LOCATION: (1020)..(1796)
FEATURE:
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NAME/KEY: CDS
LOCATION: (174)...(488)
FEATURE:
NAME/KEY: CDS
LOCATION: (528)...(977)
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Best_Local Similarity 58.6
Matches 794; Conservative
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US-09-815-242-9587
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LOCATION: (1)
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                             CCCTTCTTTACATCGGAAAACTATTTGGAGCAAAGACGATTTATATTGAAGTATTTGAT 1700
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APPLICANT: Haselbeck, Robert
APPLICANT: Haselbeck, Robert
APPLICANT: Oblsen, Kari L.

APPLICANT: Zyskind, Judith W.

APPLICANT: Zyskind, Judith W.

APPLICANT: Trawick, John D.

APPLICANT: Trawick, John D.

APPLICANT: Yamamoto, Robert T.

APPLICANT: Yamamoto, Robert T.

APPLICANT: Yu, H. Howard

TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Drokaryotes

FILE REPERENCE: ELITA.011A

CURRENT APPLICATION NUMBER: US/09/815,242

CURRENT FILING DATE: 2000-03-21

PRIOR FILING DATE: 2000-03-21

PRIOR FILING DATE: 2000-05-23
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Patent No. US20020061569A1
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Pred. No. 4.1e-50;
0; Mismatches 548;
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR PELING DATE: 2000-05-26
PRIOR PLECATION NUMBER: 60/245,578
PRIOR PLECATION NUMBER: 60/253,625
PRIOR PILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-12-22
PRIOR FILING DATE: 2001-12-22
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: PASESEQ for Windows Version 4.0
SEG ID NO 9587
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Pred. No. 1.6e-49;
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APPLICANT: GILBERT, GWENDOLYN
TITLE OF INVENTION: MOLECULAR TYPING OF GROUJ
CURRENT APPLICATION NUMBER: US/10/804,408
CURRENT FILING DATE: 2004-03-19
PRIOR APPLICATION NUMBER: PCT/AU02/01281
PRIOR PILING DATE: 2002-09-18
PRIOR FILING DATE: 2001-09-19
PRIOR FILING DATE: 2001-09-19
NUMBER OF SEQ ID NOS: 182
SOFTWARE: Patentin version 3.2
SEQ ID NO 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 178, Application US/10804408
Publication No. US20040253617A1
GENERAL INFORMATION:
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Best Local Similarity 51.9%;
Matches 1100; Conservative
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US-10-804-408-178
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US-10-804-408-178
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RESULT 25 US-10-804-408-179

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Pred. No. 8.9e-45;
0; Mismatches 975;
                                                                                                                                           OF GROUP
                                                                                                        APPLICANT: GILBERT, GWENDOLYN
TITLE OF INVENTION: MOLECULAR TYPING OF GROU
FILE REFRENCES: 675002-201
CURRENT APPLICATION NUMBER: US/10/804,408
CURRENT FILING DATE: 2004-03-19
PRIOR APPLICATION NUMBER: PCT/AU02/01281
PRIOR APPLICATION NUMBER: AU PR 7749
PRIOR FILING DATE: 2002-09-18
PRIOR FILING DATE: 2001-09-19
NUMBER OF SEQ ID NOS: 182
SOFTWARE: PatentIn version 3.2
LENGTH: 2577
Sequence 179, Application US/10804408
Publication No. US20040253617A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: DNA
; ORGANISM: Streptococcus agalactiae
US-10-804-408-179
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Best Local Similarity 51.6%;
Matches 1092; Conservative
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                                                                                    APPLICANT: FANRONG,
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3780 GAATTGCTT 1209 GTATGTTTT 3828 AGTAACGAA 1269 AGTAGTAGT 3888 ATTTTATTT 1329 TTCCTTATT		4188 ACAAAAAT 1619 4248 TGATAAAT 1665 TGAGAACTG 4308 AAATGATGG 1725 AGATGATGG	4368 AAGAATTAA 1785 TCGCGTAAA 4428 AGAACATGC 1845 TGAATGGC 4488 AATGTTCGA 1905 TATGATTGTT 1905 TATGATTGTT 1965 TTTCGA	4608 CTTAACGAG 2022 TTTCAAAA 4668 TTGGTGCAA 2082 TTGGGGGAA 4728 AAGTATTGG 2139 CAAAATTGG 4788 AGTTGATAC 2199 TGTAGATAC 4848 GAAATTCTC

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US-09-767-041-9 6992 1 atcgccaaacgaaattggca......gcaaacagcaaaagaagctt 6992 Title: Perfect score: Sequence:

IDENTITY NUC Gapox 10.0 Scoring table:

68479088 34239544 seqs, 19032134700 residues Total number of hits satisfying chosen parameters: Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

9b_est1:; 9b_htc:: 9b_est3:* 9b_est4:: 9b_est6:: 9b_gs81:* 9b_gs81:* EST:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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NO.	Score	Match	Length DB	DB	ID	Description
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. 4	2 167.4	2.4	1896	ð	CG753083	CG753083 P048-1-C0
υ	3 166.4	2.4	1592	6	CG750135	
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O	5 155.4	2.2	1626	۲	CF238805	CF238805 AGENCOURT
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• *	7 153.6	2.2	1542	0	AG386981	AG386981 Mus muscu
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0	1 146.6	2.1	1489	σ	AG350139	AG350139 Mus muscu
ä	2 144.4	2.1	1489	σ	AG350139	AG350139 Mus muscu
H	3 144	2.1	1592	σ	CG750135	CG750135 P044-3-D0
r o	4 143.4	2.1	1539	σ	AG340947	AG340947 Mus muscu
ä	5 143.2	2.0	1242	6	CL068807	CL068807 CH216-115
c C	6 143	2.0	2015	6	AG311015	AG311015 Mus muscu
-	7 143	2.0	2157	σ	CL081966	CL081966 CH216-165
ĩ	8 142.6	2.0	1594	6	CL110653	CL110653 ISB1-53P2
0	9 140.8	2.0	1608	0	CL118721	CL118721 ISB1-72J8
0	0 140	2.0	1101	9	CNSOOEVL	AL069706 Drosophil
c 5	1 139.8	2.0	1780	o	AG320553	AG320553 Mus muscu
c 5:	2 138.6	2.0	1313	7	CK997149	CK997149 ip15c02.b
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CL082000 CH216-165	AG350209 Mus muscu	CG757970 P053-2-C0	AL061936 Drosophil	CL080711 CH216-159	CC253231 CH261-180	CG749499 P043-4-A0	AG386981 Mus muscu	AG340947 Mus muscu	CG744717 P037-2-F0	CG757539 P052-4-E0	AG430010 Mus muscu	AG346840 Mus muscu	AG288305 Mus muscu	AG333887 Mus muscu	CL038406 CH216-46A	CG757503 P052-4-C0	CL466243 SAIL_1253	CL466243 SAIL_1253	CL055132 CH216-80J	CL118721 ISB1-72J8
CL082000	AG350209	CG757970	CNS0021J	CL080711	CC253231	CG749499	AG386981	AG340947	CG744717	CG757539	AG430010	AG346840	AG288305	AG333887	CL038406	CG757503	CL466243	CL466243	CL055132	CL118721
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137.6	136.2	135.8	135.4	135.4	134.2	133.8	133.8	132.6	132	131.2	130.4	130.4	130	129.8	129.4	129	128.6	127.6	127.4	127.2
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Neodiplogasteridae; Pristionchus.
Loases 1 to 1896)
Srinivasan, J., Sinz, W., Jesse, T., Wiggers-Perebolte, L., Jansen, K.,
Buntjer, J., van der Meulen, M. and Sommer, R.J.
An integrated physical and genetic map of the nematode Pristionchus
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/strain="California"
/db_xref="taxon:54126"
/clone lib="Epa EcoRI BAC Library"
/note="The library was generated by a partial digest of
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Max-Planck-Institute for Developmental Biology
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Tel: 00497071601371
Fax: 00497071601498
Email: ralf:sommer@tuebingen.mpg.de
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2.4%;
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1 (bases 1 to 1592)
Srinivasan, J., Sinz, W., Jesse, T., Wiggers-Perebolte, L., Jansen, K., Buntjer, J., van der Meulen, M. and Sommer, R.J.
An integrated physical and genetic map of the nematode Pristionchus pacificus
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Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
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3311

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1348 bp DNA linear GSS 24-OCT-2003 P043-4-A06.za Ppa EcoRI BAC Library Pristionchus pacificus genomic, genomic survey sequence.
CG749499.1 GI:37970425
GSS.
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Srinhivasan,J., Sinz,W., Jesse,T., Wiggers-Perebolte,L., Jansen,K.,
Buntjer,J., van der Meulen,M. and Sommer,R.J.
An integrated physical and genetic map of the nematode Pristionchus
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Max-Planck-Institute for Developmental Biology
Spenanustr. 37-39, Tuebingen D-72076, Germany
Faz: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
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Mol. Genet. Genomics 269 (5), 715-722 (2003)
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Neodiplogasteridae; Pristionchus.
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/clone lib="Ppa EcoRI BAC Library"
/note="The library was generated by a partial digest of the genemic DNA with EcoRI and cloning into the BAC vector."
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Pred. No. 1.6e-15;
0; Mismatches 792; Indels
                                                                          pacificus"
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
Class: BAC ends.
                                                                        /organism="Pristionchus
/mol_type="genomic DNA"
/strain="California"
                                           Location/Qualifiers
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ilarity 43.1%;
Conservative
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Euteleostomi; Pipidae;

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/dev_stage="mmbryo, stages 14-19"
/lab host="DH10B (phage-resistant)"
/clone lib="NTGD XGC Emb6"
/note="Vector: pCWV-SPORT6.1; Site 1: Not1; Site 2: EcoRV;
Cloned unidirectionally. Primer: Oligo dT. Average insert size 2.1 kb. Constructed by Invitrogen. Note: This is a Xenopus Gene Collection (XGC): library.
                                                                                                                                                                                                                                                                                        4054 CAGCACTATTTTATTTTACATCATTAGCCATATTTTTCATATAGAAACAATAGATCCGA 4113
                                                      Conteact: Daniela S. Gerhard, Ph.D.
Conteact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 RmloAD? Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Robert M. Grainger
CDNA Library Preparation. Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MCC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM14680 row: g column: 21
High quality sequence statt: 71
High quality sequence stop: 316.
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AGENCOURT 15099447 NICHD_XGC_Emb6 Xenopus tropicalis cDNA clone
IMAGE:6995950 5', mRNA sequence.
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1 (bases 1 to 1626)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, E
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea,
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    .1626
    /organism="Xenopus tropicalis"

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/clone="IMAGE:6995950"
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/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db xref="taxon:54126"
/clone_lib="Ppa EcoRI BAC Library"
/note="The library was generated by a partial digest the genomic DNA with EcoRI and cloning into the BAC vector."
                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                        15;
                                                                                                                                                                        Length 1348;
                                                                                                                                                                    Score 158; DB 9; Length 134
Pred. No. 3e-14;
0; Mismatches 631; Indels
                                                                                                                                                                      Query Match 2.3%;
Best Local Similarity 47.1%;
Matches 575; Conservative
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Cy 3729 ATAAAAAGCTAATACTAATATTTGTAATACT Db 610 ATTATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	3909 430 3969 370 4029 310 4089 250	Db	RESULT 6 CG75703 CG757503 LOCUGS DEFINITION GG757503 RECORD 1392 bp BEFINITION GG757503.1 GI:37986131 KEYWORDS SGS. SOURCE ORGANISM PRISTIONCHUS PACIFICUS SURARYCELS Mendatoda; Chrc Nechologasteridae; Pristionchus. REFERENCE 1 (bases 1 to 1392) AUTHORS STAIN'asan,J., van der Meulen,M. and TITLE Buntjer,J., van der Meulen,M. and TITLE Mol. Genet. Genomics 269 (5), 715- MEDLINE 2283591 COMMENT CONTACT: Sommer RJ BVA-Planck-Institute for Developme Spenannstr. 37-39, Tuebingen D-72C Tel: 00497071601371 FAX: 00497071601371 FAX: 00497071601371 FAX: 00497071601371 FAX: 00497071601371 FAX: 00497071601371	FEATURES Location/Qualifiers 1139 source 1139 / vyganism="Pristionchus F/mol_type="genomic DNA"
Ouery Match 2.2%; Score 155.4; DB 7; Length 1626; Best Local Similarity 42.5%; Pred. No. 7.5e-14; Matches 665; Conservative 0; Mismatches 885; Indels 15; Gaps 2; Qy 2709 TGATTTGGGGAATTTTTATGAAATGAAAAGGAAAGGGTTATTTATTTATTTATTTATT 2768 Db 1615 INTITITITITATTATTATATAAATTTTTTTTATATATAT	Db 1555	1255 TITATITITITITITITITITITITITITITITITITIT		Qy 3669 TCGCTAGCAATATATATATGCTTGTTATGGAGATATATAGGGGAAAATTTGCTTGG 3728

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, Wiggers-Perebolte,L., Jansen,K., da Sommer,R.J.
CTACTTATTATTTAAATACTGAATTGCTT 3788
                                                    AGAGAATCAAGTAACGAAGCTAGATTTATT 3848
                                                                                                                                                                    GGAAGTCATTCAGGCTATATATCATTTTT 3968
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/db xref="taxon:54126"
/clone_lib="type EcoR! BAC Library"
/note="The library was generated by a partial digest the genomic DNA with EcoR! and cloning into the BAC
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                                                                              Score 155; DB 9; Length 13
Pred. No. 8.7e-14;
0; Mismatches 683; Indels
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Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:hattori@gsc.riken.jp, URL:http://hgp.gsc.riken.go.jp/, Pel:81-45-503-911, Fax:81-45-503-9170)
Clones are derived from the mouse BAC library MSWGOL. For BAC library availability, please contact Kuniya Abe (abe@rtc.riken.jp). The Institute of Physical and Chemical Research (RIKEN) 3-1-1 Koyadai, Tsukuba, 305-0074 Japan phone: 81-298-36-9189, fax: 81-298-36-9199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AG386981 1542 bp DNA linear GSS 03-JUN-2004
Mus musculus molossinus DNA, clone:MSMg01-201G10.TJ, genomic survey
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Sciurognathi, Muridae, Murinae, Mus
CCACTACAATTATAGTTTCCATTACCGTTAATCTTTGCACTTATAAAAAATAAAATGCAAC
                                                               3364 AAAAATTAAAAATAGTATCTTTTTTAGTTTTTTAGTTTTATTAGGTATATCTGCATTGT
                                                                                                   3484 ATCTTATAACAGGCGTCAAAACAAGGTTGGTTGGCTTTATGAACTATCCTACGTTAAATA
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tori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
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1. 1542
| Organism="Mus musculus molossinus" | mol_type="genomic DNA" | sub speciees="molossinus" | db xref="taxon:57486" | /clone="MSMg01-201G10.TJ"
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BAC end Sequences of Library MSMg01
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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AUTHORS
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AUTHORS
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GSS 01-APR-2004

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Syngenta Biotechnology Inc.
3054 Cornwallis Rd., Research Triangle Park, NC 27709, USA
Bmail: allens.gessions@eyngenta.com
ABRC Stock Number CS936276; T-DNA left border flanking sequences of
Syngenta Arabidopsis Insertion Library (SAIL) lines are available
through the Arabidopsis Biological Resource Center (ABRC).
Sequences represent a pool of amplified genomic regions and not
class: TDNA tagged.
 ATATTAATTATATGCTTGTTATGGAGATATATAGGTGGAAAATTTGCTTGGATAAAAAG 3737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATAAAAAATTTCTCAGTTACAAAGAAATGGAACAATATATTAACAAATCAGAAGTAGTTA 2027
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SAIL_811_H11.v3 SAIL Collection Arabidopsis thaliana genomic clone CL509408.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

(bases 1 to 1758)
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/clone="GAIL 811 H11.v3"
/clone lib="SAIL Collection"
/note="T-DNA left border sequences were isolated using
modified TAIL-PCR strategy"
                                                                                    3618 IGTCTTGCTTTTATACCGATCTATTTAAGTGGATCGAGAATTGGTAGTTTATCGCTAGCA
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Pred. No. 3.7e-13;
0; Mismatches 1084;
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/mol_type="genomic DNA"
/ecotype="Columbia"
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                                                                                                    7;
                                                                   DB 9; Length 1542;
/tissue_type="mixture of kidney and spleen"
/clone_lib="MSMg01 Mouse Male BAC Library"
                                                                 Score 153.6; DB 9; Length
Pred. No. 1.4e-13;
0; Mismatches 664; Indels
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through the Arabidopsis Biological Resource Center (ABRC). Sequences represent a pool of amplified genomic regions and single contiguous sequences.
Class: TDNA tagged.
Location/Qualifiers
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/clone="SALL 811_H11.v3"
/clone=lb="SALL Collection"
/note="T-DNA left border sequences
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AG320553 1780 bp DNA linear GSS 02-JUN-2004 Mus msculus molossinus DNA, clone:MSMg01-106H14.TJ, genomic survey

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Direct Submission

L. Submitted (17-700*203) Masahira Hattori, The Institute of Physical
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Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the mouse BAC library MSMg01. For BAC
library availability, please contact Kuniya Abe (abe@rtc.riken.jp).
Tsukuba Institute of Physical and Chemical Research (RIKEN) 3-1-1
Koyadai, Tsukuba, 305-0074 Japan
phone: 81-298-36-9189, fax: 81-298-36-9199
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                                                            Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                    Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
BAC end Sequences of Library MSMg01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue type="mixture of kidney and spleen"
/clone_lib="MSMg01 Mouse Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Mus musculus molossinus"
/mol_type="genomic DNA"
/sub_species="molossinus"
/db_xref="taxon:57486"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2.1%; Score 148.2; DB 9;
larity 47.2%; Pred. No. 9.3e-13;
Conservative 0; Mismatches 776;
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/sex="male"
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1. .1780
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            GI:47893510
                                      musculus molossinus
musculus molossinus
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3365 3485 3544 3724 3784 3844 4024 1371 1491 3425 1552 TATATATAAAATATTTATTATATTTTATATATAGTATACTCT--ATAAATTTATATA 1609 781 841 664 721 CACTACAATTATAGTTTCAATTCCGTTAATCTTTGCACTTATAAAAATAAAATGCAACA ATTITITITITICITGTCTTGCTTTTATACCGATCTATTTAAGTGGATCGAGAATTGGTAG TTTATCGCTAGCAATATTAATTATGCTTGTTATGGAGATATATAGGTGGAAAATTTGC 1022 AFTTTTATTTTATTTTTTTAGTAATTAATTÄTATTATAATTCAAATTATÄTÄTÄT GCTTTACCATGAAATTTTGGCTGTTTATAATTCTAGAGAATCAAGTAACGAAGCTAGATT 3845 TATTATTTATCAAGGAAGTATTGATAAGTATTAGAAAACAATATTTTATTTGGATATGG ATTAACATAATTATCTTATTATTATTTTATTATTATCTACCTATCTAATTTATA **CTATTATTAAATATTATATTTATATTATAATAATAAATTATTATTATTATTAT** CT-TATAACAGGGGTCAAAACAAGGTTGGTTGGCTTTATGAACTATCCTACGTTAAATAC TIGGATAAAAAAGCTAATAGTAATATITGTAATACTACTTATTATTTTAAATACTGAATT 1314 AATATATAAA--ATAAATTATATTATATTCCATATATATTATTAATAAAATTT 4025 AAAAAAAGTTATGGAGTTAATGGGGAAACAGCACTATTTTATTTTACATTAGCCAT **ACATTACATATAATATTTATTTTCAATTAATAATATTTTATAAAATTTTGAT** 4085 ATTTTTCATATATGAACAATAGATCCGATTATTATTATTAGTACTATTCTTTTCTTC TAATTICAGITATIGIACCAATTIATAATGICCAAGATTATCTIGATAAATGIATTAACA GTATTATTAACCAAACATATACTAATTTAGAGGTTATTCTCGGTAAATGATGGAAGTACTG

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tgurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:hattorieggc.riken.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-911, Fax:81-45-503-910) (Innes are derived from the mouse BAC library MSMg01. For BAC library availability, please contact Kuniya Abe (abe@rtc.riken.jp). Trukuba Institude, Bio Resource Center, The Institute of Physical and Chemical Research (RIKEN) 3-1-1 phone: 81-298-36-9189, fax: 81-298-36-9199
                                                                                                                                                                                                                                         AG350139 1489 bp DNA linear GSS 02-JUN-2004
Mus musculus molossinus DNA, clone:MSMg01-146K14.TJ, genomic survey
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TTATGAATTCATTATCCAAAGGAAAAAAACAATTATTGTTTCCTAGACAAAAAAGTATG 2111
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
Direct Submission
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BAC end Sequences of Library MSMg01
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/clone_lib="MSMg01 Mouse Male BAC Library"
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/clone="MSMg01-146K14.TJ"
/sex="male"
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/sub_species="molossinus"
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Mus musculus molossinus
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                                                                                                                      AG350139 1489 bp DNA linear GSS 02-JUN-2004
Mus musculus molossinus DNA, clone:MSMg01-146K14.TJ, genomic survey
                                                                                                                                                                                                                                                                                                                                                          Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:hattori@gec.riken.ip, URL:http://hgp.gec.riken.go.jp/, Tel:81-45-503-911, Fax:81-45-503-9170; //hgp.gec.riken.go.jp/, Clones are derived from the mouse BAC library MSMg01. For BAC library availability, please contact Kuniya Abe (abe@rtc.riken.jp). The Institute of Physical and Chemical Research (RIKEN) 3-1-1 Koyadai, Tsukuba, 305-0074 Japan Phone: 81-298-36-9189, fax: 81-298-36-9199
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.
                                                                                                                                                                                                                                                                               Noguchi, H., Kojima, T. and Sakaki, Y
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'clone_lib="MSMg01 Mouse Male BAC Library"
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Pred. No. 3.6e-12;
0; Mismatches 699;
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BAC end Sequences of Library MSMg01
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/sub_species="molossinus"
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/clone="MSMg01-146K14.TJ"
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                                        Mus musculus molossinus
Mus musculus molossinus
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Best Local Similarity 46.7%;
Matches 643; Conservative
                          3371 AAAAAATAGTATCTTTTT
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ATCGAGCTTTTGAATACTATTTACAAAGATTGTTGTTTATTGATAGAATAAAAACATGG 2666
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                               CTTCAGAATACCTGTATAATTATTTTAAATATTCTCAGGATTTATATGTTGAATTTAACAA
                                                                                     AAGATGAGCAAAAATATAAAGAAAATAGGATAATATGAACGAGTTAAATGTTACAGATTAT
                                                                                                                TTCCTAATATATCAGAAAAACTATTGATAATGTACTGTTTAGAATTTTTAAGAATGT
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Neodiplogasteridae; Pristionchus.
1 (bases I to 1592)
2 Krinivasan, J., Sinz, W., Jesse, T., Wiggers-Perebolte, L., Jansen, K., Buntjer, J., van der Meulen, M. and Sommer, R.J.
An integrated physical and genetic map of the nematode Pristionchus
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1371 TAATTTACANTATATTATATAATAATATTTTATANCATTTATAATATTAATNTATA 1430
                                                                                                                             CG750135 1592 bp DNA linear GSS 24-OCT-2003 P044-3-D09.za Ppa EcoRI BAC Library Pristionchus pacificus genomic,
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/clone lib="pa EcoRI BAC Library"
/note="The library was generated by a partial digest
the genomic DNA with EcoRI and cloning into the BAC
vector."
                                                      TTTATTAGGTATATCTGCATTGTATTATTCAAAATGGGAAAGATATTGTATTTT
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Pred. No. 4.1e-12;
0; Mismatches 810; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                  Biology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pacificus"
                                                                                                                                                                                                                                                                                                                                                                                                    Evolutionary Biology
Max-Planck-Institute for Developmental
Spemannstr. 37-39, Tuebingen D-72076, G
Tel: 00497071601371
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Pristionchus
/mol_type="genomic DNA"
/strain="California"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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CG750135
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pacificus
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Similarity 41.3%;
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                                                                                                                                                                                                          2 (bases 1 to 1539)
Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
Direct Submission
Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2107
                         1539 bp DNA linear GSS 02-JUN-2004 DNA, clone:MSMg01-134C16.T7, genomic survey
                                                                                                                                                                                                                                                         and Chemical Research (HIKEN), Genomic Sciences Center (SSC);
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (B-mail:hattoriegger.riken.jp. URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the mouse BAC library MSMg01. For BAC library availability, please contact (kuniya Abe (abe@rtc.riken.jp). The Institute of Physical and Chemical Research (RIKEN) 3-1-1 Koyadai, Tsukuba. 305-0074 Japan
Formula 1298-36-9189, fax: 81-298-36-9199
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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                                                                                                                                                                    Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
BAC end Sequences of Library MSMg01
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1539;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue type="mixture of kidney and spleen"
/clone_lib="MSMg01 Mouse Male BAC Library"
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larity 45.5%; Pred. No. 5.1e-12;
Conservative 0; Mismatches 733;
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/mol_type="genomic DNA"
/sub_species="molossinus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:57486"
/clone="MSMg01-134C16.T7"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                       molossinus
                                                                                                        musculus molossinus
                                                                                                                    musculus molossinus
                                                                           GI:47914257
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LIBRARY
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Mus musculus
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R.Site 2
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2015 bp DNA linear GSS 02-JUN-2004 molossinus DNA, clone:MSMg01-093J24.TJ, genomic survey
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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BAC end Sequences of Library MSMg01
Upublished
2 (Danses 1 to 2015)
Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus; Silurana.

1 (bases 1 to 1242)
Mardis,C., Carter,J., McPherson,J., Warren,W., Graves,T.,
Mardis,E. and Wilson,R.
A physical map of the xenopus tropicalis genome
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /sex="male"
/cell_line="Stock 248 F7A2, inbred N7"
/clone_lib="CH216"
/note="Vector: pTARBAC2.1; CHORI-216 Xenopus tropicalis
BAC library"
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2.0%; Score 143.2; DB 9; Length 1
al Similarity 46.9%; Pred. No. 5.5e-12;
545; Conservative 0; Mismatches 613; Indels
                                                                                                                                                                                                                                                                                                                                                                Genome Sequencing Center
Washington University School of Medicine
Email: submissions@watson.wustl.edu
Insert Length: 175000 Std Error: 0.00
Seq primer: Sp6 ATTTAGGTGACACTATAG
Class: BAC ends
High quality sequence start: 7
High quality sequence stop: 57.
Location/Qualifiers
                                                                                                                                                                        Xenopus tropicalis (western clawed frog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Xenopus tropicalis"
/mol type="genomic DNA"
/strain="Nigerian frog"
/db_xref="texon:8364"
/clone="CH216-115B3"
                                                                 CL068807
CH216-115B3 Sp6.1 CH216 Xenopus tropi
CH216-115B3, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                 Contact: Richard K Wilson
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Direct Submission

Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC);

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Clones are derived from the mouse BAC library MSMg01. For BAC library availability, please contact Kuniya Abe (abe@rtc.riken.jp). Tsukuba Institute, Bio Resource Center,
The Institute of Physical and Chemical Research (RIKEN) 3-1-1

Koyadai, Tsukuba, 305-0074 Japan
phone: 81-298-36-9189, fax: 81-298-36-9199
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'clone_lib="MSMg01 Mouse Male BAC Library"
                                                                                                                                                                                                                                                                                                                         Score 143; DB 9; Length 20 Pred. No. 5.7e-12; 0; Mismatches 880; Indels
                                                                                                                                                                                                                    organism="Mus musculus molossinus"
                                                                                                                                                                                                                             /mol_type="genomic DNA"
/sub_species="molossinus"
/db_xref="taxon:57486"
                                                                                                                                                                                                                                                            clone="MSMg01-093J24.TJ"
                                                                                                                                                                                               Location/Qualifiers
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ua-09-767-041-9.rst

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3529 ATCCTACGTTAAATACCACTACAATTATAGTTTCAATTCCGTTAATCTTTGCACTTATAA 3588
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Xenopodinae; Sarnopus; Silurana.

(bases 1 to 2157)

Kremitzki, C., Carter, J., McPherson, J., Warren, W., Graves, T.,

A physical map of the xenopus tropicalis genome
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /cell_line="Stock 248 F7A2, inbred N7"
/clone_lib="CH216"
/note="Vector: pTARBAC2.1; CHORI-216 Xenopus tropicalis
BAC library"
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CH216-165D13_Sp5.1 CH216 Xenopus tropicalis genomic clone
CH216-165D13, genomic survey sequence.
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.larity 45.8%; Pred. No. 5.7e-12;
Conservative 0; Mismatches 744; Indels
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Washington University School of Medicine
Email: submissions@watson.wustl.edu
Insert Length: 175000 Std Error: 0.00
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/mol_type="genomic DNA"
/strain="Nigerian frog"
/db_xref="texon:8364"
/clone="CH216-165D13"
                                                                                                                                                                                                                                                                                                                                                                                                                            Seq primer: Sp5 atctgccgtttcgatcct
Class: BAC ends
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us-09-767-041-9.rst

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1608 bp DNA linear GSS 05-JAN-2004
Genomic survey sequence.
CL118721
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Xenopus tropicalis (western clawed frog)
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                                CL110653 1594 bp DNA linear GSS 05-JAN-2004 1SB1-53P23_Sp6.1 ISB1 Xenopus tropicalis genomic clone ISB1-53P23,
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Xenopus tropicalis

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;

Xenopodinae; Xenopus; Silurana.

1 (bases 1 to 1594)

Kremitzki, C., Carter, J., McPherson, J., Warren, W., Graves, T.,

A physical map of the xenopus tropicalis genome

Unpublished (2003)
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Library Segment 1"
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Pred. No. 6.7e-12;
0; Mismatches 729;
                                                                                                                                                                                                                                                                                                            Genome Sequencing Center
Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Xenopus tropicalis"
/mol_type="genomic DNA"
/db xref="taxon:8364"
                                                                                                                                                                                                                                                                                                                                            Email: submissions@watson.wustl.edu
Insert Length: 75000 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                   Seq primer: Sp6 ATTTAGGTGACACTATAG
Class: BAC ends
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High quality sequence start: 390
High quality sequence stop: 470.
Location/Qualifiers
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/clone lib="ISB1"
                                                                                                                                                                                                                                                                                             Contact: Richard K Wilson
                                                                   genomic survey sequence.
                                                                                              CL110653.1 GI:40604288
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Best Local Similarity 45.2%;
Matches 608; Conservative
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Drosophila melanogaster
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        fly), genomic survey sequence. ALO69706 ALO69706.1 GI:4949849 GSS.
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia: Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
Xenopodinae, Xenopus, Silurana.

1 (bases 1 to 1608)

Kremitzki, C., Carter, J., McPherson, J., Warren, W., Graves, T.,
A physical map of the xenopus tropicalis genome
Unpublished (2003)
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Library Segment 1"
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                                                                                                                                                                                                                                                                                                                                                          Score 140.8; DB 9; Length
Pred. No. 1.3e-11;
0; Mismatches 792; Indels
                                                                                                                          Genome Sequencing Center
Mashington University School of Medicine
Email: submissions@watson.wustl.edu
Insert Length: 75000 Std Error: 0.00
Seq primer: T7 TAMTACGACTCACTATAGGG
Class: BAC ends
High quality sequence start: 252
High quality sequence stop: 345.
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/organism="Xenopus tropicalis"
/mol_type="genomic DNA"
/db_xref="taxon:8364"
/clone="ISB1-7238"
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                                                                                                                Contact: Richard K Wilson
                                                                                                                                                                                                                                                                                                                                                          tch 2.0%;
al Similarity 44.6%;
644; Conservative
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CNSOOEVL 1101 bp DNA linear GSS 04-JUN-1999 Drosophila melanogaster genome survey sequence T7 end of BAC: BACR29B23 of RPCI-98 library from Drosophila melanogaster (fruit 3431 3491 3611 3851 3971 4031 4091 4151 3551 3612 TICTIGIGICTIGCTITIATACCGAICTATITAAGIGGAICGAGAATIGGIAGTITATCG 3671 8672 CTAGCAATATTAATTATATGCTTGTTATGGAGATATATAGGTGGAAAATTTGCTTGGATA 3731 AAAAAGCTAATAGTAATATTTGTAATACTACTTATTTTTAAATACTGAATTGCTTTAC 3791 TATCAAGGAAGTATTGATAAAGTATTAGAAAACAATATTTTATTTGGATATGGAATATCC 3911 338 758 278 218 936 818 698 638 578 458 158 3792 CATGAAATTTTGGCTGTTTATAATTCTAGAAATCAAGTAACGAAGCTAGATTTATTATT Tritiatatatitatatititatatititititititatatatatitatititit 3372 AAAAATAGTATCTTTTTAGTTTTTTAGTTTTAGTTATAGGTATATCTGCATTGTATATT 3432 CAAAATGGGAAAGATATTGTATTTTTAGACAGACACCTTATAGGACTAGACTATCTTATA ACAGGCGTCAAAACAAGGTTGGTTGGCTTTATGAACTATCCTACGTTAAATACCACTACA 3552 ATTATAGTTTCAATTCCGTTAATCTTTGCACTTATAAAAATAAAATGCAACAATTTTTT 3912 GAATATTCAGTTACGGGAACTTGGCTCGGAAGTCATTCAGGCTATATATCATTTTTTTAT 1092 ATATATGAAACAATAGATCCGATTATTATTATTAGTACTATTCTTTTCTTCAATAGGT

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                                                                                                                                                                                                                                                                                                                                                                            AG320553 1780 bp DNA linear GSS 02-JUN-2004
Mus musculus molossinus DNA, clone:MSMg01-106H14.TJ, genomic survey
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3387 ITTAGTTTTTAGTTTTAGTATATCTGCATTGTATATTATTCAAAATGGGAAAGAT 3446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        library availability, please contact Kuniya Abe (abe@rtc.riken.jp). Tsukuba Institude, Bio Resource Center,
The Institute of Physical and Chemical Research (RIKEN) 3-1-1
Koyadai, Tsukuba, 305-0074 Japan
phone: 81-298-36-9189, fax: 81-298-36-9199
e-mail: abe@rtc.riken.jp
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                   560 TTWWTTTAAATTATWTTTTTTTTAWTAWAWWTWAAAWAATWAWWWWAAAAATWWWWTW
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/clone_lib="MSMg01 Mouse Male BAC Library"
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BAC end Sequences of Library MSMg01
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/mub_species="molossinus"
/db_xref="taxon:57486"
/clone="MSMg01-106H14.TJ"
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1. .1780
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                                                                                                                                                                                                                      PRED: JAVOR DAY, COURT. FRANCE (E-MAIL): BEGFELGGERODECORE.CORD. TO WAVE SENDENCEDE.CORD. TO THE BAC-END SEQUENCE WAS CARRIED OUT AS PART COURT. THE BAC-END SEQUENTIA GENOME PYCJOCK (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACS. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Gsoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial ECORI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw 8p, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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                                                                                                                                                                    Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  861
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="genomic DNA"
/db_xref="taxon:7227"
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/clone_lib="RPCI-98"
/note="end : T7"
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                                                                                                                                       Direct Submission
                                                                                                    Genoscope
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/Clone lib="Brain - Cerebellum Library (DOGEST8)"
/note="Organ: Brain; Vector: pBluescript II SK; Site 1:
EcoR; Site 2: Xhol; Library constructed using pBluescript
XR kit from Stratagene. Cloned CDNA was size selected
between 1-3 kb. Mark Haskins VMD, PhD, Pathology and
Medical Genetics, School of Veterinary Medicine,
University of Pennsylvania, 3800 Spruce Street,
Philadelphia, PA 19104-6651"
                                                                                                                                                                                                                                                                                                                                                    1313 bp mRNA linear EST 26-MAR-2004 ipl5c02.bl Brain - Cerebellum Library (DOGEST8) Canis familiaris CENA clone ipl5c02, mRNA sequence.
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                                                                 1110 CCGATTATTATTATATTAGTACTATTCTTTCTTCAATAGGTATTTGGAATAATATAAAT 4169
                                                                                                                                1170 TTTAAAAAGGATATGGAGACAAAAATGAATGATTTAATTTTCAGTTATTGTACCAATTTA 4229
                                                                                                                                                                                               1230 TAATGTCCAAGATTATCTTGATAAATGTATTAACAGTATTATTAACCAAACATATACTAA 4289
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Mammalia, Eutheria, Carnivora, Fissipedia, Canidae, Canis.
                      050 GAAACAGCACTATTTTATTTTACATCATTAGCCATATTTTTCATATATGAAACAATAGAT
                                                                                                                                                               Length 1313;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue type="Cerebellum"
/dev stage="3 month old normal canine"
/lab_host="XL10 Gold"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (2004)
Contact: W. Richard McCombie
Cold Spring Hazen Genome Sequencing Center
Cold Spring Hazbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Pax: 516 367 8884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Balija,V., Nascimento,L.U. and McCombie,W.R. ESTs from Canis familiaris cerebellum (dog)
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48.5%; Pred. No. 2.8e-11;
ilve 0; Mismatches 580;

    1313
    organism="Canis familiaris"

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Plate: ipls row: c column: 02
High quality sequence stop: 1313
Location/Qualifiers
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/db_xref="taxon:9615"
/clone="ip15c02"
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Canis familiaris
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Matches 567;
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                                              ATTCCAGAGCAAAAGTATGTATTTTATTAATTTTTATGAATTTAATTTTATTTCATATA 3161
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Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:hattori@gec.riken.jb, Withthp://hgp.gsc.riken.go.jp/, Tel:81-45-503-911, Fax:81-45-503-9170)
Clones are derived from the mouse BAC library MSMg01. For BAC library availability, please contact Kuniya Abe (abe@rtc.riken.jp). Tsukuba Institude Bio Resource Center, The Institute of Physical and Chemical Research (RIKEN) 3-1-1 Koyadai, Tsukuba, 305-0074 Japan phone: 81-298-36-9189, fax: 81-298-36-9199
                                                                                                                                                                 AG338221 1745 bp DNA linear GSS 02-JUN-2004
Mus musculus molossinus DNA, clone:MSMg01-130H15.T7, genomic survey
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Direct Submission
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/clone_lib="MSMg01 Mouse Male BAC Library"
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/organism="Mus musculus molossinus"
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Pred. No. 3.1e-11;
0; Mismatches 643;
3856 AAGGAAGTATTGATAAAGTATTAGAAAACA 3885
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BAC end Sequences of Library MSMg01
Unpublished
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/sub_species="molossinus"
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/sex="male"
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Mus musculus molossinus DNA, clone:MSMg01-124L03.T7, genomic survey
                                                                                                                                                                                                                              Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.
Direct Submission
Submission
Submission
and Chemical Research (HIKEN), Genomic Sciences Center (GSC);
1-7-22 Suchiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mall:hattori@geor.riken.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the mouse BAC library MSMg01. For BAC
                                                                                                                                                                                                                                                                      Physical
                                                                                                                                                                                                                                                                                                                                                                    library availability, please contact Kuniya Abe (abe@rtc.riken.jp). Tsukuba Institude, Bio Resource Center, The Institute of Physical and Chemical Research (RIKEN) 3-1-1 Koyadai, Tsukuba, 305-0074 Japan phone: 81-298-36-9189, fax: 81-298-36-9199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1851 AATAATAATAATAAAAATAATAATAATGATTGATATATCATATAATAATAATGATAAATG 1792
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                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                Kojima, T. and Sakaki, Y
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="mixture of kidney and spleen'
/clone_lib="MSMg01 Mouse Male BAC Library"
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45.7%; Pred. No. 3.6e-11;
tive 0; Mismatches 947;
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Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="genomic DNA"
/sub_species="molossinus"
/db_xref="taxon:57486"
/clone="WSMg01-124L03.T7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                 Mus musculus molossinus
Mus musculus molossinus
                                                  GI:47907293
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Vector : pBAC
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                                  2704 CCACATGATTTTGTGGCAATTCTTTTATCAAATGAAAACGAAACAGCTTATTTTAAG 2763
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2392 TCATCTTCTCTCAGGAGAATGCACCATTAGTTCCTTCAGAATACCTGTATAATTATTT 2451

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1611 TAAT-TTATATACTAATTATAATTTAATGTTTAATTTATATTTAAATTTAGAGAATA 1553

TATACCGATC 3638

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CH216-165P18 RM4.1 CH216 Xenopus tropicalis genomic clone CH216-165P18, genomic survey sequence.
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3519 TITAIGAACTATCCTACGTTAAAIACCACTACAATTATAGTTTCAATTCCGTTAATCTTT 3578
                                                                                                                                                                                                                                                                                                                                                   3817 CTAGAGAATCAAGTAACGAAGCTAGATTTATTATTATCAAGGAAGTATTGATAAAGTAT 3876
                                                                                                 368 TIATITIATIAATTAGATTAATTAAATATATAAATTAAAATTTATATATATATTAATC 309
                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopoulinae; Xenopus; Silurana.

1 (bases 1 to 1981)

Kremitzki, C., Carter, J., McPherson, J., Warren, W., Graves, T., Mardis, E. and Wilson, R.

A physical map of the xenopus tropicalis genome
Unpublished (2003)
                                                                                                                                      CTACTTATTATTTAAATACTGA--ATTGCTTTACCATGAAATTTTGGCTGTTTATAATT
                                                                 3579 GCACTTATAAAAATAAATGCAACAATTTTTTTTTTTGTGTGTTTG
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Pred. No. 3.8e-11;
0; Mismatches 876;
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Genome Sequencing Center
Washington University School of Medicine
Email: submissions@watson.wustl.edu
Email: submissions@watson.wustl.edu
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Xenopus tropicalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Xenopus tropicalis"
/mol_type="genomic DNA"
/strain="Nigerian frog"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seq primer: RM ctcaagggcatcggtcgagc
Class: BAC ends
High quality sequence start: 265
High quality sequence stop: 497.
Location/Qualifiers
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/clone="CH216-165P18"
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GSS.
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Best Local Similarity 43.4%;
Matches 674; Conservative
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/cell line=
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              TAAATATTCTCAGGATTTATATGTTGAATTTACAAAAGATGAGCAAAAATATAAAGAAAA
                                                                               TAGGATATATGAACGAGTTAAATGTTACAGATTATTTCCTAATATATCAGAAAAAACTAT
                                                                                                                  AGAACATTATATTATTATTAATAATATCTATAAATGTÁTCTÁTTÁTATATGATTAA
                                                                                                                                                    TGATAATGTACTGTTTAGAATTTTAATGAATGTATCGAGCTTTTGAATACTATTTACA
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3831 AACGAAGCTAGATTTATTATTATCAAGGAAGTATTGATAAAGTATTAGAAAACAATATT 3890 3891 TTATTTGGATATGGAATATCCGAATATTCAGTTACGGGAACTTGGCTCGGAAGTCATTCA 3950 3951 GGCTATATATCATTTTTTTTATAATCAGGAATAGTTGGGTTGATTTTTACTGATGTTTTCT 4010 4071 ACATCATTAGCCATATTTTTCATATAGAACAATAGATCCGATTATTATTAGTA 4130 4191 AAAAATGAATTTAATTTCAGTTATTGTACCAATTTATAATGTCCAAGATTATCTTGA 4250 1165 İTATITITATITITATITITAAİTTATITITITATITITATITITATITITATITIACTT 4251 TAAATGTATTAACAGTATTATTAACCAAACATATACTAATTTAGAGGTTATTCT 4304 ò 엄 ò g Š 셤 **상** 원 8 6 요 ò õ

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